

Sequence: 1 CLLS 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 891005

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*

1: geneseqp1980s:*

2: geneseqp1990s:*

3: geneseqp2000s:*

4: geneseqp2001s:*

5: geneseqp2002s:*

6: geneseqp2003as:*

7: geneseqp2003bs:*

8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	%		DB	ID	Description
		Query	Match Length			
1	21	100.0	4	4	AAB70004	Aab70004 Human CD4
2	21	100.0	6	4	AAB70006	Aab70006 Mammalian
3	21	100.0	6	4	AAB70008	Aab70008 Mammalian
4	21	100.0	6	4	AAB73336	Aab73336 Peptide #
5	21	100.0	7	4	AAG98813	Aag98813 Human cel
6	21	100.0	8	4	AAB70015	Aab70015 Mammalian
7	21	100.0	9	5	ABJ04568	Abj04568 Bone marr
8	21	100.0	9	5	ABB90512	Abb90512 Hominidae
9	21	100.0	9	6	ABR75290	Abr75290 Biologica
10	21	100.0	10	4	AAM98000	Aam98000 Human pep
11	21	100.0	10	6	ABR83453	Abr83453 HLA epito
12	21	100.0	11	4	AAB45734	Aab45734 Human 7TM
13	21	100.0	11	6	ABR83452	Abr83452 HLA epito
14	21	100.0	12	2	AAW32645	Aaw32645 Human pla
15	21	100.0	12	2	AAW09530	Aaw09530 Thrombopo
16	21	100.0	12	2	AAW35435	Aaw35435 Thrombopo
17	21	100.0	12	2	AAW36681	Aaw36681 Thrombopo
18	21	100.0	12	2	AAW71775	Aaw71775 Mimotope
19	21	100.0	12	4	AAU25900	Aau25900 Human thr
20	21	100.0	12	4	AAB70016	Aab70016 Mammalian
21	21	100.0	12	6	ABR83451	Abr83451 HLA epito
22	21	100.0	13	6	ABR83450	Abr83450 HLA epito

23	21	100.0	14	2	AAY08370
24	21	100.0	14	4	AAM98606
25	21	100.0	14	6	ABR83449
26	21	100.0	15	5	ABP59178
27	21	100.0	15	5	ABP58957
28	21	100.0	15	5	AAM52614
29	21	100.0	15	6	ABB98938
30	21	100.0	15	6	ABR83448
31	21	100.0	16	4	AAB70014
32	21	100.0	16	5	ABJ00630
33	21	100.0	16	5	ABG33491
34	21	100.0	17	6	ABO32586
35	21	100.0	17	6	AAO23254
36	21	100.0	18	4	AAG98812
37	21	100.0	19	3	AAB51759
38	21	100.0	19	4	AAB87126
39	21	100.0	20	4	AAB76364
40	21	100.0	20	4	AAB76367
41	21	100.0	20	5	ABJ15277
42	21	100.0	21	3	AAB09109
43	21	100.0	21	3	AAB29839
44	21	100.0	21	4	AAE05263
45	21	100.0	21	4	AAB89248

Aay08370	Cysteine
Aam98606	Human pep
Abr83449	HLA epito
Abp59178	Human pho
Abp58957	Human zin
Aam52614	Human YSK
Abb98938	Zinc fing
Abr83448	HLA epito
Aab70014	Mammalian
Abj00630	B lymphoc
Abg33491	B Lymphoc
Abo32586	Secreted
Aao23254	GBV-B cor
Aag98812	Human cel
Aab51759	Human sec
Aab87126	Human MAN
Aab76364	ErbB2 bin
Aab76367	ErbB2 bin
Abj15277	IGF relat
Aab09109	Hepatitis
Aab29839	Human sec
Aae05263	Mouse par
Aab89248	HIV gp120

Sequence: 1 CLLS 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 264921

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*

- 1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
- 2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
- 3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
- 4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
- 5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
- 6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	21	100.0	7	3	US-09-461-697-431	Sequence 431, App
2	21	100.0	12	2	US-08-406-330-23	Sequence 23, Appl
3	21	100.0	12	2	US-08-764-640-86	Sequence 86, Appl
4	21	100.0	12	2	US-08-556-597-23	Sequence 23, Appl
5	21	100.0	12	3	US-08-973-225-86	Sequence 86, Appl
6	21	100.0	12	3	US-08-973-225-210	Sequence 210, App
7	21	100.0	12	3	US-09-244-298A-86	Sequence 86, Appl
8	21	100.0	12	3	US-09-516-704-86	Sequence 86, Appl
9	21	100.0	12	4	US-09-549-090-86	Sequence 86, Appl
10	21	100.0	12	4	US-09-549-090-210	Sequence 210, App
11	21	100.0	12	4	US-09-832-230A-86	Sequence 86, Appl
12	21	100.0	18	3	US-09-461-697-429	Sequence 429, App
13	21	100.0	21	4	US-08-469-260A-231	Sequence 231, App
14	21	100.0	21	4	US-08-488-446-231	Sequence 231, App
15	21	100.0	21	4	US-08-467-344A-231	Sequence 231, App
16	21	100.0	22	1	US-08-039-778B-2	Sequence 2, Appli
17	21	100.0	23	2	US-08-902-516-15	Sequence 15, Appl
18	21	100.0	23	4	US-09-847-185-15	Sequence 15, Appl
19	21	100.0	24	4	US-09-716-129-156	Sequence 156, App
20	21	100.0	27	1	US-08-039-778B-1	Sequence 1, Appli
21	21	100.0	31	1	US-08-053-131-91	Sequence 91, Appl
22	21	100.0	31	1	US-08-645-641-91	Sequence 91, Appl
23	21	100.0	31	1	US-07-853-408B-91	Sequence 91, Appl
24	21	100.0	31	2	US-08-096-762-91	Sequence 91, Appl

25	21	100.0	31	2	US-08-308-865-91	Sequence 91, Appl
26	21	100.0	31	3	US-09-042-353-288	Sequence 288, App
27	21	100.0	31	4	US-08-758-417A-136	Sequence 136, App
28	21	100.0	31	5	PCT-US92-10983-91	Sequence 91, Appl
29	21	100.0	35	4	US-09-227-357-228	Sequence 228, App
30	21	100.0	36	2	US-08-411-098-15	Sequence 15, Appl
31	21	100.0	37	4	US-09-060-299-10	Sequence 10, Appl
32	21	100.0	37	4	US-09-402-923A-10	Sequence 10, Appl
33	21	100.0	38	4	US-09-060-299-9	Sequence 9, Appli
34	21	100.0	38	4	US-09-402-923A-9	Sequence 9, Appli
35	21	100.0	39	4	US-09-060-299-16	Sequence 16, Appl
36	21	100.0	39	4	US-09-402-923A-16	Sequence 16, Appl
37	21	100.0	41	1	US-08-548-540-94	Sequence 94, Appl
38	21	100.0	41	4	US-09-904-615-112	Sequence 112, App
39	21	100.0	41	5	PCT-US96-09809-94	Sequence 94, Appl
40	21	100.0	44	2	US-08-766-858A-14	Sequence 14, Appl
41	21	100.0	45	1	US-08-548-540-93	Sequence 93, Appl
42	21	100.0	45	1	US-08-542-363-18	Sequence 18, Appl
43	21	100.0	45	3	US-09-100-089-18	Sequence 18, Appl
44	21	100.0	45	4	US-09-670-827-18	Sequence 18, Appl
45	21	100.0	45	5	PCT-US96-09809-93	Sequence 93, Appl

Sequence: 1 CLLS 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1276540 seqs, 311283816 residues

Total number of hits satisfying chosen parameters: 533274

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
- 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	21	100.0	4	9	US-09-929-924-2	Sequence 2, Appli
2	21	100.0	6	9	US-09-929-924-4	Sequence 4, Appli
3	21	100.0	6	9	US-09-929-924-6	Sequence 6, Appli
4	21	100.0	7	9	US-09-922-261-431	Sequence 431, App
5	21	100.0	8	9	US-09-929-924-13	Sequence 13, Appl
6	21	100.0	9	14	US-10-254-446A-143	Sequence 143, App
7	21	100.0	9	16	US-10-333-068-146	Sequence 146, App
8	21	100.0	10	9	US-09-952-432A-12	Sequence 12, Appl
9	21	100.0	10	15	US-10-026-066-20	Sequence 20, Appl
10	21	100.0	11	14	US-10-116-252-44	Sequence 44, Appl
11	21	100.0	11	15	US-10-026-066-19	Sequence 19, Appl
12	21	100.0	12	9	US-09-929-924-14	Sequence 14, Appl

13	21	100.0	12	14	US-10-083-768-86	Sequence 86, Appl
14	21	100.0	12	14	US-10-083-768-210	Sequence 210, App
15	21	100.0	12	15	US-10-026-066-18	Sequence 18, Appl
16	21	100.0	13	15	US-10-026-066-17	Sequence 17, Appl
17	21	100.0	14	15	US-10-026-066-16	Sequence 16, Appl
18	21	100.0	15	15	US-10-026-066-15	Sequence 15, Appl
19	21	100.0	16	9	US-09-929-924-12	Sequence 12, Appl
20	21	100.0	16	10	US-09-932-613-88	Sequence 88, Appl
21	21	100.0	16	10	US-09-932-322-88	Sequence 88, Appl
22	21	100.0	17	10	US-09-759-130B-184	Sequence 184, App
23	21	100.0	17	16	US-10-741-790-184	Sequence 184, App
24	21	100.0	18	9	US-09-922-261-429	Sequence 429, App
25	21	100.0	20	14	US-10-098-093-53	Sequence 53, Appl
26	21	100.0	20	14	US-10-196-394-15	Sequence 15, Appl
27	21	100.0	20	14	US-10-196-394-18	Sequence 18, Appl
28	21	100.0	21	8	US-08-424-550B-231	Sequence 231, App
29	21	100.0	21	9	US-09-754-997A-44	Sequence 44, Appl
30	21	100.0	21	14	US-10-084-813-354	Sequence 354, App
31	21	100.0	21	14	US-10-084-813-355	Sequence 355, App
32	21	100.0	21	14	US-10-084-813-356	Sequence 356, App
33	21	100.0	21	15	US-10-026-066-14	Sequence 14, Appl
34	21	100.0	23	9	US-09-847-185-15	Sequence 15, Appl
35	21	100.0	23	10	US-09-962-756-1105	Sequence 1105, Ap
36	21	100.0	23	14	US-10-224-286-15	Sequence 15, Appl
37	21	100.0	23	15	US-10-253-471-1105	Sequence 1105, Ap
38	21	100.0	23	16	US-10-253-493-1105	Sequence 1105, Ap
39	21	100.0	24	12	US-10-632-983-156	Sequence 156, App
40	21	100.0	26	14	US-10-029-386-29995	Sequence 29995, A
41	21	100.0	27	9	US-09-864-761-45459	Sequence 45459, A
42	21	100.0	27	10	US-09-974-879-343	Sequence 343, App
43	21	100.0	27	10	US-09-305-736-343	Sequence 343, App
44	21	100.0	27	11	US-09-818-683-343	Sequence 343, App
45	21	100.0	27	12	US-10-621-401-343	Sequence 343, App

Sequence: 1 CLLS 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 37674

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		%					
No.	Score	Query	Match	Length	DB	ID	Description
1	21	100.0	34	2	H81600	hypothetical prote	
2	21	100.0	36	2	S17834	acetyl-CoA carboxy	
3	21	100.0	36	2	B53480	T-cell receptor al	
4	21	100.0	42	2	I55360	ornithine-oxo-acid	
5	21	100.0	45	2	G82146	hypothetical prote	
6	21	100.0	62	2	S25999	hypothetical prote	
7	21	100.0	64	2	H70210	hypothetical prote	
8	21	100.0	65	2	C82569	hypothetical prote	
9	21	100.0	70	1	XISR1A	insect toxin 1 - S	
10	21	100.0	70	1	S08267	toxin 1 - scorpion	
11	21	100.0	72	2	A36379	lymphotoxin C1 pre	
12	21	100.0	77	2	AE2043	hypothetical prote	
13	21	100.0	83	2	B42525	A-ORF-O protein -	
14	21	100.0	85	1	D65088	murein-lipoprotein	
15	21	100.0	85	2	D69069	hypothetical prote	
16	21	100.0	88	2	G34444	insect toxin 2 pre	
17	21	100.0	88	2	B90855	hypothetical prote	
18	21	100.0	90	2	H87544	hypothetical prote	
19	21	100.0	93	2	A86491	CT001 hypothetical	
20	21	100.0	93	2	F72130	conserved hypothet	
21	21	100.0	98	2	S36062	Ig lambda chain -	
22	19	90.5	15	2	PH1455	T-cell receptor al	
23	19	90.5	36	2	B27633	Ig lambda-2 chain	
24	19	90.5	37	1	Q6BP37	gene 6.3 protein -	
25	19	90.5	43	2	B82527	hypothetical prote	
26	19	90.5	44	2	D90673	hypothetical prote	

27	19	90.5	54	2	AF3462	hypothetical prote
28	19	90.5	62	2	A90849	cell division inhi
29	19	90.5	62	2	D90914	inhibitor of cell
30	19	90.5	65	2	D33172	C-ORF-E protein -
31	19	90.5	65	2	E83492	hypothetical prote
32	19	90.5	65	2	B97869	Na ⁺ /H ⁺ antiporter
33	19	90.5	66	2	A28644	kappa-neurotoxin -
34	19	90.5	67	2	I54754	integrin beta 7 su
35	19	90.5	67	2	E90798	hypothetical prote
36	19	90.5	68	2	T21285	hypothetical prote
37	19	90.5	68	2	AB2736	hypothetical prote
38	19	90.5	78	2	D81246	hypothetical prote
39	19	90.5	78	2	S43287	H ⁺ -transporting AT
40	19	90.5	79	2	A82875	ribosomal protein
41	19	90.5	80	2	H89990	hypothetical prote
42	19	90.5	81	2	C89872	hypothetical prote
43	19	90.5	82	2	I57802	Ig lambda2-like ch
44	19	90.5	83	2	S07941	proteinase inhibit
45	19	90.5	84	2	H86827	hypothetical prote

Sequence: 1 CLLS 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 15046

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		%				
No.	Score	Query Match	Length	DB	ID	Description
1	21	100.0	55	1	E1A6_ADE02	P24934 human adeno
2	21	100.0	62	1	YM32_MARPO	P38474 marchantia
3	21	100.0	70	1	SIX1_LEIQU	P19856 leiurus qui
4	21	100.0	83	1	YVAO_VACCC	P20524 vaccinia vi
5	21	100.0	85	1	YQHH_ECOLI	Q46860 escherichia
6	21	100.0	88	1	SIX1_ANDAU	P01497 androctonus
7	21	100.0	88	1	SIX1_MESMA	O61668 mesobuthus
8	21	100.0	88	1	SIX2_ANDAU	P15147 androctonus
9	21	100.0	92	1	PLM_MOUSE	Q9z239 mus musculu
10	21	100.0	92	1	PLM_RAT	O08589 rattus norv
11	19	90.5	37	1	Y63_BPT7	P03799 bacteriopha
12	19	90.5	65	1	YVCE_VACCC	P21123 vaccinia vi
13	19	90.5	66	1	NXL2_BUNFL	P15815 bungarus fl
14	19	90.5	69	1	GBGU_HUMAN	O14610 homo sapien
15	19	90.5	73	1	YKFH_ECOLI	Q9xb42 escherichia
16	19	90.5	79	1	RS18_UREPA	Q9ppt8 ureaplasma
17	19	90.5	83	1	IBB3_SOYBN	P01064 glycine max
18	19	90.5	85	1	V042_FOWPV	Q9j5g1 fowlpox vir
19	19	90.5	87	1	NXL1_BUNMU	P01398 bungarus mu
20	19	90.5	87	1	NXL3_BUNMU	P15817 bungarus mu
21	19	90.5	87	1	NXL4_BUNMU	O12961 bungarus mu
22	19	90.5	87	1	NXL5_BUNMU	O12962 bungarus mu
23	19	90.5	91	1	VE5A_HPVI1	P04017 human papil
24	19	90.5	91	1	VE5A_HPVI6	P20970 human papil
25	19	90.5	99	1	YGAV_ECOLI	P77295 escherichia
26	18	85.7	30	1	CX2A_CONBE	P58625 conus betul
27	18	85.7	32	1	CAL0_BOVIN	P01260 bos taurus
28	18	85.7	32	1	CAL0_PIG	P01259 sus scrofa
29	18	85.7	33	1	RRPO_BPBZ1	P09674 bacteriopha
30	18	85.7	40	1	BD10_BOVIN	P46168 bos taurus

31	18	85.7	55	1	TP75_TREPA	Q01305	treponema p
32	18	85.7	57	1	RIC1_PHYIN	Q9y068	phytophthor
33	18	85.7	71	1	VG71_BPPF3	P03628	bacterioph
34	18	85.7	73	1	YCZF_BACSU	O31479	bacillus su
35	18	85.7	75	1	MIH_PROCL	P55848	procambarus
36	18	85.7	76	1	CEMA_VICFA	P20864	vicia faba
37	18	85.7	78	1	THGF_HELAN	P82659	helianthus
38	18	85.7	78	1	YDH2_PLAFS	P14588	plasmodium
39	18	85.7	79	1	LEUD_NEIGO	Q50974	neisseria g
40	18	85.7	79	1	YD06_LISMO	Q92c47	listeria mo
41	18	85.7	79	1	YNBE_LACLA	Q9cg27	lactococcus
42	18	85.7	80	1	SCX1_TITSE	P01496	tityus serr
43	18	85.7	80	1	SCX4_TITSE	P45659	tityus serr
44	18	85.7	85	1	SC10_MESMA	Q9njc5	mesobuthus
45	18	85.7	92	1	CLP9_DROME	P82384	drosophila

Sequence: 1 CLLS 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 175362

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_25:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		%	Query					
No.	Score	Match	Length	DB	ID	Description		
1	21	100.0	29	8	Q9G5Z4	Q9g5z4 pseudocalot		
2	21	100.0	34	16	Q9K2B9	Q9k2b9 chlamydia p		
3	21	100.0	35	4	Q96RX9	Q96rx9 homo sapien		
4	21	100.0	35	16	Q98NE6	Q98ne6 rhizobium l		
5	21	100.0	37	2	Q9X9E9	Q9x9e9 uncultured		
6	21	100.0	37	2	Q9X9F0	Q9x9f0 uncultured		
7	21	100.0	37	5	Q9TYA1	Q9tya1 reticuliter		
8	21	100.0	41	4	Q9Y3F8	Q9y3f8 homo sapien		
9	21	100.0	45	16	Q9KQW6	Q9kqw6 vibrio chol		
10	21	100.0	47	4	Q8N341	Q8n341 homo sapien		
11	21	100.0	53	4	Q9BYL8	Q9byl8 homo sapien		
12	21	100.0	54	3	Q07058	Q07058 saccharomyc		
13	21	100.0	55	2	Q847N8	Q847n8 aster yello		

14	21	100.0	57	12	Q8JJW7	Q8jjw7 sweet potat
15	21	100.0	59	12	Q91PQ2	Q91pq2 tt virus. o
16	21	100.0	64	16	O50925	O50925 borrelia bu
17	21	100.0	65	16	Q9PAY9	Q9pay9 xylella fas
18	21	100.0	67	13	Q98TK8	Q98tk8 platichthys
19	21	100.0	68	12	Q84155	Q84155 orf virus (
20	21	100.0	70	10	Q9LDA6	Q9lda6 oryza sativ
21	21	100.0	71	6	Q8HY42	Q8hy42 bos taurus
22	21	100.0	71	6	Q8HY28	Q8hy28 ovis aries
23	21	100.0	72	4	Q86W78	Q86w78 homo sapien
24	21	100.0	72	12	Q9J7S7	Q9j7s7 tt virus. o
25	21	100.0	72	12	Q80B03	Q80b03 orf virus.
26	21	100.0	73	5	Q8IFD3	Q8ifd3 trypanosoma
27	21	100.0	73	16	Q8F5M2	Q8f5m2 leptospira
28	21	100.0	74	4	O95358	O95358 homo sapien
29	21	100.0	74	5	Q86EX4	Q86ex4 schistosoma
30	21	100.0	74	12	Q9JF32	Q9jf32 vaccinia vi
31	21	100.0	75	17	Q8PWP4	Q8pwp4 methanosarc
32	21	100.0	76	5	Q95RQ0	Q95rq0 drosophila
33	21	100.0	76	8	Q7YIX7	Q7yix7 marsilea qu
34	21	100.0	77	16	Q8YVS5	Q8yvs5 anabaena sp
35	21	100.0	78	2	Q8GFU4	Q8gfu4 citrobacter
36	21	100.0	78	4	Q9P1I3	Q9pli3 homo sapien
37	21	100.0	79	13	Q9DGB1	Q9dgb1 oryzias lat
38	21	100.0	79	16	Q931M3	Q931m3 staphylococ
39	21	100.0	81	5	Q8MWC1	Q8mwcl1 penaeus mon
40	21	100.0	81	5	O97410	O97410 anopheles g
41	21	100.0	82	5	Q8MMP5	Q8mmp5 penaeus mon
42	21	100.0	83	5	Q8IH83	Q8ih83 drosophila
43	21	100.0	83	12	Q9JF58	Q9jf58 vaccinia vi
44	21	100.0	84	4	Q9NTR9	Q9ntr9 homo sapien
45	21	100.0	85	16	Q8CVQ5	Q8cvq5 escherichia

Title: US-09-929-924-4
Perfect score: 37
Sequence: 1 WQCLLS 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 891005

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		%					
No.	Score	Query	Match	Length	DB	ID	Description
1	37	100.0	6	4	AAB70006	Aab70006	Mammalian
2	37	100.0	8	4	AAB70015	Aab70015	Mammalian
3	37	100.0	12	4	AAB70016	Aab70016	Mammalian
4	37	100.0	16	4	AAB70014	Aab70014	Mammalian
5	37	100.0	21	4	AAB89248	Aab89248	HIV gp120
6	37	100.0	21	4	AAB89247	Aab89247	HIV gp120
7	37	100.0	21	4	AAB89249	Aab89249	HIV gp120
8	37	100.0	72	4	AAB70019	Aab70019	Mammalian
9	37	100.0	73	4	AAB70018	Aab70018	Mammalian
10	35	94.6	73	4	AAB70029	Aab70029	Human CD4
11	35	94.6	73	4	AAB70028	Aab70028	Human CD4
12	32	86.5	25	4	AAM21523	Aam21523	Peptide #
13	32	86.5	25	4	ABB43868	Abb43868	Peptide #
14	32	86.5	25	4	AAM37783	Aam37783	Peptide #
15	32	86.5	25	4	ABB26794	Abb26794	Protein #
16	32	86.5	25	4	AAM77595	Aam77595	Human bon
17	32	86.5	25	4	AAM64852	Aam64852	Human bra
18	32	86.5	25	4	ABG59245	Abg59245	Human liv
19	32	86.5	25	5	ABG46629	Abg46629	Human pep
20	32	86.5	55	3	AAG02892	Aag02892	Human sec

21	32	86.5	71	4	AAU44569	Aau44569	Propionib
22	32	86.5	71	6	ABM41088	Abm41088	Propionib
23	32	86.5	73	4	AAB70025	Aab70025	Human CD4
24	31	83.8	6	4	AAB70008	Aab70008	Mammalian
25	31	83.8	31	4	AAM19115	Aam19115	Peptide #
26	31	83.8	31	4	AAM31764	Aam31764	Peptide #
27	31	83.8	31	5	ABG41275	Abg41275	Human pep
28	31	83.8	51	4	AAU56911	Aau56911	Propionib
29	31	83.8	51	6	ABM53430	Abm53430	Propionib
30	31	83.8	73	4	AAB70026	Aab70026	Human CD4
31	31	83.8	73	4	AAB70027	Aab70027	Human CD4
32	31	83.8	75	4	AAU86644	Aau86644	Novel hum
33	31	83.8	75	7	ADB59978	Adb59978	Connectiv
34	30	81.1	6	4	AAB70009	Aab70009	Mammalian
35	30	81.1	24	2	AAY12811	Aay12811	Human 5'
36	30	81.1	34	4	AAE01734	Aae01734	Human gen
37	30	81.1	34	4	AAE01688	Aae01688	Human gen
38	30	81.1	34	5	ABG63992	Abg63992	Human alb
39	30	81.1	34	5	ABG63991	Abg63991	Human alb
40	30	81.1	53	6	ABP99903	Abp99903	Breast sp
41	30	81.1	60	4	ABB14935	Abb14935	Human ner
42	30	81.1	66	3	AAG01769	Aag01769	Human sec
43	30	81.1	67	4	AAU56577	Aau56577	Propionib
44	30	81.1	67	6	ABM53096	Abm53096	Propionib
45	30	81.1	71	3	AAG59775	Aag59775	Arabidops

Title: US-09-929-924-4
 Perfect score: 37
 Sequence: 1 WQCLLS 6

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 264921

Minimum DB seq length: 0
 Maximum DB seq length: 100

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Issued_Patents_AA:*
 1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
 2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
 3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
 4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
 5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
 6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	37	100.0	83	2	US-08-332-562A-87	Sequence 87, Appl
2	29	78.4	10	2	US-08-406-330-16	Sequence 16, Appl
3	29	78.4	10	2	US-08-556-597-16	Sequence 16, Appl
4	29	78.4	77	4	US-09-621-976-5778	Sequence 5778, Ap
5	29	78.4	98	2	US-08-248-839C-131	Sequence 131, App
6	28	75.7	90	2	US-08-557-309B-24	Sequence 24, Appl
7	28	75.7	90	3	US-08-834-306-24	Sequence 24, Appl
8	28	75.7	90	3	US-08-993-674A-24	Sequence 24, Appl
9	28	75.7	90	4	US-09-256-976-24	Sequence 24, Appl
10	28	75.7	91	4	US-09-134-001C-5571	Sequence 5571, Ap
11	27	73.0	8	3	US-08-444-818-449	Sequence 449, App
12	27	73.0	8	3	US-08-444-818-450	Sequence 450, App
13	27	73.0	8	3	US-08-444-818-451	Sequence 451, App
14	27	73.0	21	3	US-08-867-611-55	Sequence 55, Appl
15	27	73.0	21	4	US-09-257-179-91	Sequence 91, Appl
16	27	73.0	21	4	US-09-690-359-55	Sequence 55, Appl
17	27	73.0	54	4	US-09-418-710-46	Sequence 46, Appl
18	27	73.0	54	4	US-09-418-710-59	Sequence 59, Appl
19	27	73.0	55	4	US-09-621-976-6709	Sequence 6709, Ap
20	27	73.0	63	4	US-09-252-991A-23832	Sequence 23832, A
21	27	73.0	98	4	US-09-716-129-81	Sequence 81, Appl
22	26	70.3	9	2	US-08-126-016-19	Sequence 19, Appl

23	26	70.3	11	4	US-09-069-827A-36	Sequence 36, Appl
24	26	70.3	13	2	US-08-126-016-23	Sequence 23, Appl
25	26	70.3	13	3	US-09-258-754-105	Sequence 105, App
26	26	70.3	13	3	US-09-042-107-105	Sequence 105, App
27	26	70.3	13	4	US-09-722-250D-105	Sequence 105, App
28	26	70.3	16	1	US-08-444-231-21	Sequence 21, Appl
29	26	70.3	16	1	US-08-152-443A-21	Sequence 21, Appl
30	26	70.3	20	1	US-08-484-135-59	Sequence 59, Appl
31	26	70.3	20	1	US-08-484-635-230	Sequence 230, App
32	26	70.3	20	2	US-08-484-631-230	Sequence 230, App
33	26	70.3	20	2	US-08-827-570-230	Sequence 230, App
34	26	70.3	21	1	US-08-526-710-16	Sequence 16, Appl
35	26	70.3	21	1	US-08-484-635-96	Sequence 96, Appl
36	26	70.3	21	2	US-08-484-631-96	Sequence 96, Appl
37	26	70.3	21	2	US-08-827-570-96	Sequence 96, Appl
38	26	70.3	21	3	US-08-862-855-16	Sequence 16, Appl
39	26	70.3	21	3	US-09-226-985-16	Sequence 16, Appl
40	26	70.3	21	4	US-09-227-906-16	Sequence 16, Appl
41	26	70.3	22	1	US-08-484-635-141	Sequence 141, App
42	26	70.3	22	1	US-08-484-635-156	Sequence 156, App
43	26	70.3	22	2	US-08-484-631-141	Sequence 141, App
44	26	70.3	22	2	US-08-484-631-156	Sequence 156, App
45	26	70.3	22	2	US-08-827-570-141	Sequence 141, App

Title: US-09-929-924-4
Perfect score: 37
Sequence: 1 WQCLLS 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1276540 seqs, 311283816 residues

Total number of hits satisfying chosen parameters: 533274

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
- 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	37	100.0	6	9	US-09-929-924-4	Sequence 4, Appli
2	37	100.0	8	9	US-09-929-924-13	Sequence 13, Appl
3	37	100.0	12	9	US-09-929-924-14	Sequence 14, Appl
4	37	100.0	16	9	US-09-929-924-12	Sequence 12, Appl
5	37	100.0	21	14	US-10-084-813-354	Sequence 354, App
6	37	100.0	21	14	US-10-084-813-355	Sequence 355, App
7	37	100.0	21	14	US-10-084-813-356	Sequence 356, App
8	37	100.0	72	9	US-09-929-924-17	Sequence 17, Appl
9	37	100.0	73	9	US-09-929-924-16	Sequence 16, Appl
10	35	94.6	73	9	US-09-929-924-36	Sequence 36, Appl

11	35	94.6	73	9	US-09-929-924-37	Sequence 37, Appl
12	33	89.2	40	14	US-10-029-386-28338	Sequence 28338, A
13	33	89.2	74	12	US-10-424-599-195133	Sequence 195133,
14	33	89.2	75	12	US-10-424-599-229210	Sequence 229210,
15	33	89.2	76	16	US-10-437-963-143360	Sequence 143360,
16	33	89.2	83	16	US-10-437-963-132784	Sequence 132784,
17	33	89.2	96	12	US-10-424-599-152706	Sequence 152706,
18	32	86.5	25	9	US-09-864-761-42092	Sequence 42092, A
19	32	86.5	29	14	US-10-029-386-29404	Sequence 29404, A
20	32	86.5	66	12	US-10-424-599-249329	Sequence 249329,
21	32	86.5	73	9	US-09-929-924-33	Sequence 33; Appl
22	31	83.8	6	9	US-09-929-924-6	Sequence 6, Appli
23	31	83.8	31	9	US-09-864-761-48187	Sequence 48187, A
24	31	83.8	59	12	US-10-424-599-165784	Sequence 165784,
25	31	83.8	62	12	US-10-424-599-246412	Sequence 246412,
26	31	83.8	70	16	US-10-437-963-156831	Sequence 156831,
27	31	83.8	73	9	US-09-929-924-34	Sequence 34, Appl
28	31	83.8	73	9	US-09-929-924-35	Sequence 35, Appl
29	31	83.8	75	9	US-09-764-847-709	Sequence 709, App
30	31	83.8	75	14	US-10-092-154-709	Sequence 709, App
31	31	83.8	99	12	US-10-424-599-216059	Sequence 216059,
32	30	81.1	6	9	US-09-929-924-7	Sequence 7, Appli
33	30	81.1	22	14	US-10-190-082-622	Sequence 622, App
34	30	81.1	34	11	US-09-833-245-738	Sequence 738, App
35	30	81.1	34	11	US-09-833-245-739	Sequence 739, App
36	30	81.1	53	14	US-10-082-828A-184	Sequence 184, App
37	30	81.1	54	12	US-10-424-599-223359	Sequence 223359,
38	30	81.1	62	12	US-10-424-599-171255	Sequence 171255,
39	30	81.1	65	12	US-10-424-599-271554	Sequence 271554,
40	30	81.1	66	12	US-10-424-599-248985	Sequence 248985,
41	30	81.1	75	16	US-10-437-963-105429	Sequence 105429,
42	30	81.1	79	13	US-10-001-835-199	Sequence 199, App
43	30	81.1	82	9	US-09-925-299-936	Sequence 936, App
44	30	81.1	82	9	US-09-867-550-1308	Sequence 1308, Ap
45	30	81.1	82	10	US-09-925-299-936	Sequence 936, App

Sequence: 1 WQCLLS 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 37674

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	%		DB	ID	Description
		Query	Match Length			
1	31	83.8	98	2	T18099	hypothetical prote
2	29	78.4	30	2	I52254	gene CYP11B2 prote
3	29	78.4	62	2	S22564	finger protein - h
4	29	78.4	73	2	AE3264	hypothetical prote
5	29	78.4	79	2	S24379	hypothetical prote
6	29	78.4	82	2	S74971	transposase ssr269
7	29	78.4	97	2	F82416	hypothetical prote
8	29	78.4	100	2	S76444	transposase slr016
9	29	78.4	100	2	S76090	transposase sll016
10	28	75.7	57	2	S30502	protein-tyrosine k
11	28	75.7	57	2	E82667	hypothetical prote
12	28	75.7	96	2	T05760	hypothetical prote
13	27	73.0	55	2	H82976	rubredoxin PA5350
14	27	73.0	55	2	A82977	rubredoxin PA5351
15	27	73.0	87	2	C85825	hypothetical prote
16	27	73.0	87	2	F90979	hypothetical prote
17	27	73.0	88	2	H91290	hypothetical prote
18	27	73.0	94	2	E96562	unknown protein, 7
19	26	70.3	33	2	B58512	bromosleeper pepti
20	26	70.3	39	2	I46149	aldolase A - dog (
21	26	70.3	39	2	I57685	aldolase A - south
22	26	70.3	43	2	I45824	aldolase C - New Z
23	26	70.3	43	2	I46150	aldolase C - dog (
24	26	70.3	43	2	I77472	aldolase - Gnypeto
25	26	70.3	52	2	D96609	hypothetical prote
26	26	70.3	57	2	PQ0401	genome polyprotein

27	26	70.3	73	2	AF2302	hypothetical prote
28	26	70.3	77	2	AE2043	hypothetical prote
29	25	67.6	29	2	C61233	conceptus protein
30	25	67.6	29	2	A55891	delta-conotoxin Gm
31	25	67.6	46	2	D97456	hypothetical prote
32	25	67.6	52	1	A33173	rubredoxin [valida
33	25	67.6	54	2	S40406	blt101 protein - b
34	25	67.6	56	2	AB2413	hypothetical prote
35	25	67.6	59	2	F87558	rubredoxin [import
36	25	67.6	72	2	G64130	hypothetical prote
37	25	67.6	79	2	AE2788	hypothetical prote
38	25	67.6	83	2	E75218	ribosomal protein
39	25	67.6	86	2	B71204	ribosomal protein
40	25	67.6	90	2	AI2914	hypothetical prote
41	25	67.6	90	2	D97689	hypothetical prote
42	25	67.6	96	2	E70811	hypothetical prote
43	25	67.6	97	2	S59427	hypothetical prote
44	24	64.9	43	2	D82489	hypothetical prote
45	24	64.9	46	2	A41814	somatotropin recep

Title: US-09-929-924-4
Perfect score: 37
Sequence: 1 WQCLLS 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 15046

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Query Match %	Length	DB	ID	Description
1	27	73.0	17	1	CXMA_CONPE	P58926 conus penna
2	26	70.3	33	1	CXBW_CONRA	P58804 conus radia
3	26	70.3	52	1	RC21_ARATH	Q9fe70 arabidopsis
4	26	70.3	69	1	TOX1_OXYKI	P83288 oxyopes kit
5	25	67.6	29	1	CXD6_CONGL	Q9twm7 conus glori
6	25	67.6	31	1	PETN_CYACA	Q9tlr6 cyanidium c
7	25	67.6	52	1	RUBR_CLOTS	P19500 clostridium
8	25	67.6	54	1	LT01_HORVU	Q42509 hordeum vul
9	25	67.6	54	1	LT02_HORVU	Q9ard5 hordeum vul
10	25	67.6	72	1	YF77_HAEIN	Q57070 haemophilus
11	25	67.6	80	1	R37A_THEAC	Q9hip0 thermoplasm
12	25	67.6	83	1	R37A_PYRAB	Q9v202 pyrococcus
13	25	67.6	83	1	R37A_PYRFU	Q8tzi4 pyrococcus
14	25	67.6	83	1	R37A_PYRHO	O74106 pyrococcus
15	25	67.6	85	1	SWM2_MOUSE	Q9jhy3 mus musculu
16	25	67.6	95	1	R37A_HALN1	Q9hsg8 halobacteri
17	24	64.9	19	1	CXR_CONTU	P58811 conus tulip
18	24	64.9	49	1	LYC_PSEPE	P21776 pseudocheir
19	24	64.9	89	1	BARS_BACAM	P11540 bacillus am
20	24	64.9	100	1	UCR9_EUGGR	P43266 euglena gra
21	23	62.2	30	1	CX2A_CONBE	P58625 conus betul
22	23	62.2	36	1	YRKG_BACSU	P54434 bacillus su
23	23	62.2	50	1	Y900_MYCTU	Q10558 mycobacteri
24	23	62.2	52	1	RUBR_TREPA	O83956 treponema p
25	23	62.2	54	1	RC2B_ARATH	Q9zns6 arabidopsis
26	23	62.2	70	1	SIX1_LEIQU	P19856 leiurus qui
27	23	62.2	85	1	DYL1_SCHPO	Q9ur05 schizosacch
28	23	62.2	88	1	SIX1_ANDAU	P01497 androctonus

29	23	62.2	88	1	SIX2_ANDAU	P15147	androctonus
30	23	62.2	89	1	CFA_CITFR	P45509	citrobacter
31	23	62.2	89	1	DYL1_ANTCR	O02414	anthocidari
32	23	62.2	89	1	DYL1_CAEEL	Q22799	caenorhabdi
33	23	62.2	89	1	DYL1_DROME	Q24117	drosophila
34	23	62.2	89	1	DYL1_HUMAN	Q15701	homo sapien
35	23	62.2	89	1	DYL1_SCHMA	Q94758	schistosoma
36	23	62.2	89	1	DYL2_DROME	O96860	drosophila
37	23	62.2	89	1	DYL2_SCHMA	Q94748	schistosoma
38	23	62.2	89	1	DYLL_HUMAN	Q9y3p0	homo sapien
39	23	62.2	91	1	DYL1_CHLRE	Q39580	chlamydomon
40	23	62.2	97	1	VMT2_IACKB	P36348	influenza a
41	23	62.2	97	1	VMT2_IAFPW	P05778	influenza a
42	23	62.2	97	1	VMT2_IAMAN	P08382	influenza a
43	22	59.5	19	1	LANA_ACTLG	P56650	actinoplane
44	22	59.5	37	1	REV_SIVM2	P08809	simian immu
45	22	59.5	37	1	TXP3_APTSC	P49268	aptostichus

Title: US-09-929-924-4
Perfect score: 37
Sequence: 1 WQCLLS 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 175362

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_25:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertibrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result						Description
	No.	Score	% Match	Query Length	DB ID	
1	37	100.0	71	6	Q8HY42	Q8hy42 bos taurus
2	37	100.0	71	6	Q8HY28	Q8hy28 ovis aries
3	37	100.0	90	11	P70443	P70443 mus musculu
4	31	83.8	98	12	O41079	O41079 paramecium
5	29	78.4	30	11	Q80XW1	Q80xw1 rattus sp.
6	29	78.4	52	5	Q8IEZ0	Q8iez0 trypanosoma
7	29	78.4	73	16	Q8YJI5	Q8yji5 brucella me
8	29	78.4	78	5	P90569	P90569 plasmodium
9	29	78.4	78	6	Q28373	Q28373 equus cabal
10	29	78.4	79	2	Q02306	Q02306 pseudomonas
11	29	78.4	81	4	Q96HL5	Q96hl5 homo sapien

12	29	78.4	82	16	P72992	P72992 synechocyst
13	29	78.4	90	5	Q9BII1	Q9bii1 anopheles g
14	29	78.4	92	16	Q8XTF4	Q8xtf4 ralstonia s
15	29	78.4	94	5	Q9U706	Q9u706 plasmodium
16	29	78.4	94	5	Q9U705	Q9u705 plasmodium
17	29	78.4	94	5	Q9U708	Q9u708 plasmodium
18	29	78.4	94	5	Q9U709	Q9u709 plasmodium
19	29	78.4	95	5	Q9U704	Q9u704 plasmodium
20	29	78.4	95	5	Q9U711	Q9u711 plasmodium
21	29	78.4	95	5	Q9U710	Q9u710 plasmodium
22	29	78.4	95	5	Q9U707	Q9u707 plasmodium
23	29	78.4	95	5	Q9U712	Q9u712 plasmodium
24	29	78.4	96	5	O61170	O61170 plasmodium
25	29	78.4	97	5	Q9U703	Q9u703 plasmodium
26	29	78.4	97	5	Q9U702	Q9u702 plasmodium
27	29	78.4	97	16	Q9KLF2	Q9klf2 vibrio chol
28	29	78.4	100	16	P74472	P74472 synechocyst
29	29	78.4	100	16	Q55567	Q55567 synechocyst
30	28	75.7	36	12	O40961	O40961 little cher
31	28	75.7	38	2	Q8KWH7	Q8kwh7 lactobacill
32	28	75.7	43	16	Q8EI27	Q8ei27 shewanella
33	28	75.7	52	4	Q9UD86	Q9ud86 homo sapien
34	28	75.7	54	4	Q9UD37	Q9ud37 homo sapien
35	28	75.7	55	16	Q88C68	Q88c68 pseudomonas
36	28	75.7	55	16	Q87U41	Q87u41 pseudomonas
37	28	75.7	57	16	Q9PD38	Q9pd38 xylella fas
38	28	75.7	57	16	Q7UNI6	Q7uni6 rhodopirell
39	28	75.7	69	13	Q9I894	Q9i894 oncorhynchu
40	28	75.7	74	2	P72426	P72426 staphylococ
41	28	75.7	78	16	Q8CTB8	Q8ctb8 staphylococ
42	28	75.7	96	10	O81839	O81839 arabidopsis
43	27	73.0	8	6	O02831	O02831 oryctolagus
44	27	73.0	21	4	Q9BQF3	Q9bqf3 homo sapien
45	27	73.0	46	15	Q9WLZ9	Q9wlz9 mouse endog

Title: US-09-929-924-5
Perfect score: 32
Sequence: 1 WQALLS 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 891005

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		%					
No.	Score	Query	Match	Length	DB	ID	Description
1	32	100.0	6	4	AAB70007	Aab70007	Mammalian
2	29	90.6	10	7	ADD94620	Add94620	Human SIM
3	29	90.6	20	2	AAW27325	Aaw27325	Human Myt
4	29	90.6	22	4	AAM22056	Aam22056	Peptide #
5	29	90.6	22	4	ABB44449	Abb44449	Peptide #
6	29	90.6	22	4	AAM38437	Aam38437	Peptide #
7	29	90.6	22	4	ABB27288	Abb27288	Protein #
8	29	90.6	22	4	AAM78194	Aam78194	Human bon
9	29	90.6	22	4	AAM65533	Aam65533	Human bra
10	29	90.6	22	4	ABG59835	Abg59835	Human liv
11	29	90.6	22	5	ABG47196	Abg47196	Human pep
12	29	90.6	57	5	ABP34364	Abp34364	Human ORF
13	29	90.6	70	4	AAM23587	Aam23587	Human EST
14	28	87.5	6	4	AAB70006	Aab70006	Mammalian
15	28	87.5	8	4	AAB70015	Aab70015	Mammalian
16	28	87.5	12	4	AAB70016	Aab70016	Mammalian
17	28	87.5	16	4	AAB70014	Aab70014	Mammalian
18	28	87.5	17	2	AAR67130	Aar67130	Factor Xa
19	28	87.5	21	4	AAB89248	Aab89248	HIV gp120
20	28	87.5	21	4	AAB89247	Aab89247	HIV gp120

21	28	87.5	21	4	AAB89249	Aab89249	HIV gp120
22	28	87.5	29	2	AAY08892	Aay08892	Chimeric
23	28	87.5	38	7	ADB48034	Adb48034	Novel hum
24	28	87.5	52	3	AAG56482	Aag56482	Arabidops
25	28	87.5	52	3	AAG58744	Aag58744	Arabidops
26	28	87.5	58	4	AAU60983	Aau60983	Propionib
27	28	87.5	58	6	ABM57502	Abm57502	Propionib
28	28	87.5	65	4	AAU22351	Aau22351	Human car
29	28	87.5	65	7	ADE46319	Ade46319	Human car
30	28	87.5	72	4	AAB70019	Aab70019	Mammalian
31	28	87.5	73	4	AAB70018	Aab70018	Mammalian
32	27	84.4	20	5	AAU88545	Aau88545	Insulin/i
33	27	84.4	20	5	AAU90912	Aau90912	Insulin/i
34	27	84.4	20	6	ADA04596	Ada04596	Insulin r
35	27	84.4	20	6	ADA03392	Ada03392	Insulin r
36	27	84.4	23	5	AAU90690	Aau90690	Insulin/i
37	27	84.4	23	5	AAU88261	Aau88261	Insulin/i
38	27	84.4	23	6	ADA04526	Ada04526	IR/IGF-1R
39	27	84.4	43	4	AAM19110	Aam19110	Peptide #
40	27	84.4	43	4	ABB38319	Abb38319	Peptide #
41	27	84.4	43	4	AAM31760	Aam31760	Peptide #
42	27	84.4	43	4	AAM58935	Aam58935	Human bra
43	27	84.4	43	4	ABG53157	Abg53157	Human liv
44	27	84.4	43	5	ABG41270	Abg41270	Human pep
45	27	84.4	44	4	AAM21284	Aam21284	Peptide #

Title: US-09-929-924-5
Perfect score: 32
Sequence: 1 WQALLS 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 264921

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	29	90.6	20	2	US-09-067-379-8	Sequence 8, Appli
2	29	90.6	20	3	US-09-067-506-8	Sequence 8, Appli
3	28	87.5	17	2	US-08-934-222-123	Sequence 123, App
4	28	87.5	17	2	US-08-933-402-123	Sequence 123, App
5	28	87.5	17	2	US-09-207-621-123	Sequence 123, App
6	28	87.5	17	2	US-08-532-818-123	Sequence 123, App
7	28	87.5	17	3	US-09-231-797-123	Sequence 123, App
8	28	87.5	17	3	US-08-934-224-123	Sequence 123, App
9	28	87.5	17	3	US-08-933-843-123	Sequence 123, App
10	28	87.5	17	3	US-08-934-223-123	Sequence 123, App
11	28	87.5	17	3	US-09-413-492-123	Sequence 123, App
12	28	87.5	83	2	US-08-332-562A-87	Sequence 87, Appl
13	28	87.5	99	2	US-09-047-125-7	Sequence 7, Appli
14	28	87.5	99	2	US-09-047-125-8	Sequence 8, Appli
15	28	87.5	99	3	US-07-736-335E-7	Sequence 7, Appli
16	28	87.5	99	3	US-07-736-335E-8	Sequence 8, Appli
17	26	81.2	26	2	US-08-967-999-11	Sequence 11, Appl
18	26	81.2	100	4	US-09-025-596-74	Sequence 74, Appl
19	26	81.2	100	4	US-09-073-661-74	Sequence 74, Appl
20	26	81.2	100	4	US-10-100-785-74	Sequence 74, Appl
21	25	78.1	17	1	US-08-333-565-12	Sequence 12, Appl
22	25	78.1	17	2	US-08-661-479-12	Sequence 12, Appl

23	25	78.1	18	3	US-08-460-576-6	Sequence 6, Appli
24	25	78.1	20	1	US-08-029-402-3	Sequence 3, Appli
25	25	78.1	23	1	US-08-029-402-17	Sequence 17, Appl
26	25	78.1	80	4	US-09-543-681A-5692	Sequence 5692, Ap
27	24	75.0	8	3	US-08-160-604-72	Sequence 72, Appl
28	24	75.0	15	2	US-08-592-646A-58	Sequence 58, Appl
29	24	75.0	15	4	US-09-165-422-58	Sequence 58, Appl
30	24	75.0	15	4	US-09-347-504-35	Sequence 35, Appl
31	24	75.0	15	4	US-10-161-499-35	Sequence 35, Appl
32	24	75.0	16	2	US-08-934-222-130	Sequence 130, App
33	24	75.0	16	2	US-08-934-222-131	Sequence 131, App
34	24	75.0	16	2	US-08-933-402-130	Sequence 130, App
35	24	75.0	16	2	US-08-933-402-131	Sequence 131, App
36	24	75.0	16	2	US-09-207-621-130	Sequence 130, App
37	24	75.0	16	2	US-09-207-621-131	Sequence 131, App
38	24	75.0	16	2	US-08-532-818-130	Sequence 130, App
39	24	75.0	16	2	US-08-532-818-131	Sequence 131, App
40	24	75.0	16	3	US-09-231-797-130	Sequence 130, App
41	24	75.0	16	3	US-09-231-797-131	Sequence 131, App
42	24	75.0	16	3	US-08-934-224-130	Sequence 130, App
43	24	75.0	16	3	US-08-934-224-131	Sequence 131, App
44	24	75.0	16	3	US-08-933-843-130	Sequence 130, App
45	24	75.0	16	3	US-08-933-843-131	Sequence 131, App

Title: US-09-929-924-5
Perfect score: 32
Sequence: 1 WQALLS 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1276540 seqs, 311283816 residues

Total number of hits satisfying chosen parameters: 533274

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
- 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	32	100.0	6	9	US-09-929-924-5	Sequence 5, Appli
2	29	90.6	22	9	US-09-864-761-42586	Sequence 42586, A
3	29	90.6	55	16	US-10-437-963-188665	Sequence 188665,
4	29	90.6	57	11	US-09-864-408A-6674	Sequence 6674, Ap
5	28	87.5	6	9	US-09-929-924-4	Sequence 4, Appli
6	28	87.5	8	9	US-09-929-924-13	Sequence 13, Appl
7	28	87.5	12	9	US-09-929-924-14	Sequence 14, Appl
8	28	87.5	16	9	US-09-929-924-12	Sequence 12, Appl
9	28	87.5	21	14	US-10-084-813-354	Sequence 354, App
10	28	87.5	21	14	US-10-084-813-355	Sequence 355, App

11	28	87.5	21	14	US-10-084-813-356	Sequence 356, App
12	28	87.5	22	14	US-10-029-386-31731	Sequence 31731, A
13	28	87.5	38	10	US-09-774-639-268	Sequence 268, App
14	28	87.5	38	10	US-09-969-730-317	Sequence 317, App
15	28	87.5	38	16	US-10-621-363-317	Sequence 317, App
16	28	87.5	59	16	US-10-437-963-175795	Sequence 175795,
17	28	87.5	60	16	US-10-437-963-176476	Sequence 176476,
18	28	87.5	65	9	US-09-764-869-1125	Sequence 1125, Ap
19	28	87.5	65	14	US-10-091-504-1125	Sequence 1125, Ap
20	28	87.5	65	15	US-10-227-577-1125	Sequence 1125, Ap
21	28	87.5	69	16	US-10-437-963-111113	Sequence 111113,
22	28	87.5	72	9	US-09-929-924-17	Sequence 17, Appl
23	28	87.5	73	9	US-09-929-924-16	Sequence 16, Appl
24	28	87.5	74	12	US-10-424-599-211217	Sequence 211217,
25	27	84.4	20	10	US-09-962-756-23	Sequence 23, Appl
26	27	84.4	20	10	US-09-962-756-1227	Sequence 1227, Ap
27	27	84.4	20	15	US-10-253-471-23	Sequence 23, Appl
28	27	84.4	20	15	US-10-253-471-1227	Sequence 1227, Ap
29	27	84.4	20	16	US-10-253-493-23	Sequence 23, Appl
30	27	84.4	20	16	US-10-253-493-1227	Sequence 1227, Ap
31	27	84.4	23	10	US-09-962-756-1157	Sequence 1157, Ap
32	27	84.4	23	14	US-10-029-386-30956	Sequence 30956, A
33	27	84.4	23	15	US-10-253-471-1157	Sequence 1157, Ap
34	27	84.4	23	16	US-10-253-493-1157	Sequence 1157, Ap
35	27	84.4	43	9	US-09-864-761-43437	Sequence 43437, A
36	27	84.4	44	9	US-09-864-761-41869	Sequence 41869, A
37	27	84.4	59	9	US-09-867-550-980	Sequence 980, App
38	27	84.4	66	12	US-10-424-599-254253	Sequence 254253,
39	27	84.4	75	12	US-10-424-599-198447	Sequence 198447,
40	27	84.4	77	12	US-10-424-599-264886	Sequence 264886,
41	27	84.4	85	16	US-10-437-963-115561	Sequence 115561,
42	27	84.4	86	9	US-09-864-761-42654	Sequence 42654, A
43	27	84.4	92	9	US-09-354-453-40	Sequence 40, Appl
44	27	84.4	92	14	US-10-267-718-40	Sequence 40, Appl
45	26	81.2	20	14	US-10-148-671-1	Sequence 1, Appli

Title: US-09-929-924-5
 Perfect score: 32
 Sequence: 1 WQALLS 6

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 37674

Minimum DB seq length: 0
 Maximum DB seq length: 100

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : PIR_78:*
 1: pir1:*
 2: pir2:*
 3: pir3:*
 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		%					
Result		Query					
No.	Score	Match	Length	DB	ID	Description	
1	27	84.4	87	2	C85825	hypothetical prote	
2	27	84.4	87	2	F90979	hypothetical prote	
3	26	81.2	47	2	G82712	hypothetical prote	
4	25	78.1	73	2	H95898	hypothetical prote	
5	25	78.1	94	2	H71549	probable trp opero	
6	24	75.0	46	2	S11162	photosystem II pro	
7	24	75.0	46	2	A41814	somatotropin recep	
8	24	75.0	52	2	A95046	hypothetical prote	
9	24	75.0	52	2	H97916	hypothetical prote	
10	24	75.0	59	2	T07432	photosystem II pro	
11	24	75.0	61	1	F2RZKS	photosystem II pro	
12	24	75.0	61	2	S02115	photosystem II pro	
13	24	75.0	61	2	S28768	photosystem II pro	
14	24	75.0	61	2	S31447	photosystem II pro	
15	24	75.0	61	2	S58534	photosystem II pro	
16	24	75.0	62	2	T02777	y4dN protein - Rhi	
17	24	75.0	95	2	H69767	hypothetical prote	
18	24	75.0	97	2	AH0965	probable secreted	
19	24	75.0	98	1	F2NTK	photosystem II pro	
20	24	75.0	100	2	C72775	hypothetical prote	
21	23	71.9	36	2	I38913	histidyl-tRNA synt	
22	23	71.9	42	2	T07294	photosystem II pro	
23	23	71.9	44	2	I65485	IR protein - Esche	
24	23	71.9	50	2	B60718	phospholipase A2 h	

25	23	71.9	52	2	D82588	hypothetical prote
26	23	71.9	55	2	A05024	photosystem II pro
27	23	71.9	64	2	A86551	CT382.1 hypothetic
28	23	71.9	64	2	A72074	hypothetical prote
29	23	71.9	69	2	S28195	tissue kallikrein
30	23	71.9	69	2	S14074	hypothetical prote
31	23	71.9	69	2	AG3599	transcription regu
32	23	71.9	72	2	S28196	tissue kallikrein
33	23	71.9	74	2	D87195	hypothetical prote
34	23	71.9	75	1	S74973	virulence associat
35	23	71.9	79	2	F95210	conserved domain p
36	23	71.9	82	2	D82577	hypothetical prote
37	23	71.9	82	2	A98165	insertion element
38	23	71.9	82	2	G98128	insertion element
39	23	71.9	84	2	A89984	hypothetical prote
40	23	71.9	88	2	F82487	hypothetical prote
41	23	71.9	90	2	S29941	late embryogenesis
42	23	71.9	93	2	AD2047	hypothetical prote
43	23	71.9	100	2	E32302	chemotaxis protein
44	22	68.8	32	2	E82279	hypothetical prote
45	22	68.8	38	2	T01741	hypothetical prote

Title: US-09-929-924-5
Perfect score: 32
Sequence: 1 WQALLS 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 15046

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		%					
No.	Score	Query	Match	Length	DB	ID	Description
1	26	81.2	90	1	Y941	COXBU	Q83d06 coxiella bu
2	25	78.1	94	1	TRPR	CHLTR	O84171 chlamydia t
3	25	78.1	98	1	FA10	NOTSC	P82807 notechis sc
4	24	75.0	37	1	REV	SIVM2	P08809 simian immu
5	24	75.0	46	1	PSBK	CHLRE	P18263 chlamydomon
6	24	75.0	46	1	PSBK	NEPOL	Q9tky7 nephroselmi
7	24	75.0	56	1	PSBK	PINTH	P41598 pinus thunb
8	24	75.0	58	1	PSBK	CHAGL	Q8ma00 chaetosphae
9	24	75.0	58	1	PSBK	PSINU	Q8wi34 psilotum nu
10	24	75.0	59	1	PSBK	OENHO	Q9mt16 oenothera h
11	24	75.0	59	1	PSBK	SPIOL	P12163 spinacia ol
12	24	75.0	61	1	PSBK	ARATH	P56782 arabidopsis
13	24	75.0	61	1	PSBK	HORVU	P25877 hordeum vul
14	24	75.0	61	1	PSBK	LOTJA	Q9bbs2 lotus japon
15	24	75.0	61	1	PSBK	MAIZE	P48188 zea mays (m
16	24	75.0	61	1	PSBK	ORYSA	P12162 oryza sativ
17	24	75.0	61	1	PSBK	SINAL	P10347 sinapis alb
18	24	75.0	61	1	PSBK	TOBAC	P12164 nicotiana t
19	24	75.0	61	1	PSBK	WHEAT	P58273 triticum ae
20	24	75.0	62	1	Y4DN	RHISN	P55413 rhizobium s
21	24	75.0	89	1	CFA	CITFR	P45509 citrobacter
22	24	75.0	95	1	YCZJ	BACSU	O31484 bacillus su
23	24	75.0	99	1	MDCC	KLEPN	O32712 klebsiella
24	23	71.9	42	1	PSBK	CHLVU	P56348 chlorella v
25	23	71.9	47	1	PSBK	MESVI	Q9mus0 mesostigma
26	23	71.9	55	1	PSBK	MARPO	P10348 marchantia
27	23	71.9	69	1	YFXX	AZOCA	P26486 azorhizobiu
28	23	71.9	91	1	YP54	XANAC	Q8pjh7 xanthomonas

29	23	71.9	92	1	YO19_XANCP	Q8p829	xanthomonas
30	23	71.9	100	1	CHER_ENTAE	P21824	enterobacte
31	22	68.8	74	1	YDCE_ECO57	Q8x9x8	escherichia
32	22	68.8	76	1	YDCE_ECOLI	P31992	escherichia
33	22	68.8	83	1	Y9KD_BPBF2	P19195	bacterioph
34	22	68.8	85	1	Y522_PSEAE	Q51483	pseudomonas
35	22	68.8	87	1	CYC6_EUGGR	P00119	euglena gra
36	22	68.8	92	1	FELA_FELCA	P30438	felis silve
37	22	68.8	94	1	Y882_MYCTU	Q10544	mycobacteri
38	22	68.8	95	1	CILG_HAEIN	P44461	haemophilus
39	22	68.8	99	1	YQJK_ECOLI	Q47710	escherichia
40	22	68.8	100	1	REV_SIVSP	P19502	simian immu
41	21	65.6	29	1	PETN_CYAPA	P48258	cyanophora
42	21	65.6	29	1	PETN_GUITH	O78498	guillardia
43	21	65.6	29	1	PETN_PORPU	P51276	porphyra pu
44	21	65.6	44	1	PSBK_ODOSI	P49513	odontella s
45	21	65.6	45	1	PSBK_CYAPA	P14237	cyanophora

Title: US-09-929-924-5
Perfect score: 32
Sequence: 1 WQALLS 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 175362

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_25:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp Vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriaphage:*
17: sp_archaeophages:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		%					Description
Result	Query	Match	Length	DB	ID		
No.	Score						
1	29	90.6	42	16	Q8FZI7	Q8fzi7 brucella su	
2	29	90.6	68	8	Q8HJX2	Q8hjsx2 ascobulla f	
3	28	87.5	54	17	Q8ZZF6	Q8zzf6 pyrobaculum	
4	28	87.5	55	10	Q84QN7	Q84qn7 oryza sativ	
5	28	87.5	71	6	Q8HY42	Q8hy42 bos taurus	
6	28	87.5	71	6	Q8HY28	Q8hy28 ovis aries	
7	28	87.5	88	16	Q88ZR0	Q88zr0 lactobacill	
8	28	87.5	90	11	P70443	P70443 mus musculu	
9	27	84.4	58	16	Q8CLT7	Q8clt7 yersinia pe	
10	27	84.4	66	17	Q8ZZX5	Q8zzx5 pyrobaculum	
11	27	84.4	87	16	Q8X8U6	Q8x8u6 escherichia	

12	26	81.2	42	8	Q34478	Q34478 euperipatoi
13	26	81.2	47	16	Q9PE35	Q9pe35 xylella fas
14	26	81.2	52	16	Q8EGW9	Q8egw9 shewanella
15	26	81.2	69	8	Q8WfY2	Q8wfy2 discorsopag
16	26	81.2	69	14	Q99IS8	Q99is8 uncultured
17	26	81.2	83	2	P77431	P77431 escherichia
18	26	81.2	84	2	Q93EH7	Q93eh7 helicobacte
19	26	81.2	99	8	Q37764	Q37764 mytilus edu
20	25	78.1	21	13	Q9PS60	Q9ps60 gallus gall
21	25	78.1	40	6	Q9TRU3	Q9tru3 oryctolagus
22	25	78.1	52	16	Q7U5T8	Q7u5t8 synechococc
23	25	78.1	54	16	Q87U84	Q87u84 pseudomonas
24	25	78.1	59	9	Q9MCU1	Q9mcu1 bacterioph
25	25	78.1	65	8	Q36125	Q36125 thyrophygus
26	25	78.1	73	16	Q92W89	Q92w89 rhizobium m
27	25	78.1	81	4	Q7Z6Q0	Q7z6q0 homo sapien
28	25	78.1	83	9	Q7Y4I7	Q7y4i7 streptococc
29	25	78.1	83	17	Q8ZUV8	Q8zuv8 pyrobaculum
30	25	78.1	84	16	Q98EA2	Q98ea2 rhizobium l
31	25	78.1	89	17	Q8ZXS8	Q8zxs8 pyrobaculum
32	25	78.1	94	2	Q8KQD7	Q8kqd7 chlamydia t
33	25	78.1	94	2	Q8KQD4	Q8kqd4 chlamydia t
34	25	78.1	100	2	Q8VML0	Q8vml0 pseudomonas
35	25	78.1	100	11	Q8C8G5	Q8c8g5 mus musculu
36	24	75.0	14	6	O77538	O77538 bos taurus
37	24	75.0	17	15	Q73442	Q73442 human immun
38	24	75.0	18	8	Q9GB22	Q9gb22 calyptomena
39	24	75.0	21	4	Q9UQV9	Q9uqv9 homo sapien
40	24	75.0	23	4	Q9HCW9	Q9hcw9 homo sapien
41	24	75.0	27	8	Q8SFG9	Q8sfg9 tachycineta
42	24	75.0	27	8	Q8SFG8	Q8sfg8 tachycineta
43	24	75.0	27	8	Q8SFG7	Q8sfg7 tachycineta
44	24	75.0	27	8	Q8SFG4	Q8sfg4 tachycineta
45	24	75.0	27	8	Q8SFH1	Q8sfh1 progne subi

Title: US-09-929-924-9
Perfect score: 25
Sequence: 1 VVQVVA 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 891005

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		%	Query				
No.	Score	Match	Length	DB	ID	Description	
1	25	100.0	6	4	AAB70021	Aab70021 Murine D4	
2	25	100.0	6	4	AAB70011	Aab70011 Mammalian	
3	25	100.0	12	4	AAB70017	Aab70017 Mammalian	
4	25	100.0	72	4	AAB70019	Aab70019 Mammalian	
5	24	96.0	10	5	AAE26314	Aae26314 Human rBP	
6	22	88.0	50	3	AAY65385	Aay65385 Human 5'	
7	22	88.0	52	4	AAU64643	Aau64643 Propionib	
8	22	88.0	52	6	ABM61162	Abm61162 Propionib	
9	22	88.0	58	4	AAU39860	Aau39860 Propionib	
10	22	88.0	58	6	ABM36379	Abm36379 Propionib	
11	22	88.0	88	4	AAU62887	Aau62887 Propionib	
12	22	88.0	88	6	ABM59406	Abm59406 Propionib	
13	21	84.0	8	3	AAB08552	Aab08552 Peptide i	
14	21	84.0	9	2	AAW43751	Aaw43751 Bacterici	
15	21	84.0	16	3	AAB08553	Aab08553 Peptide i	
16	21	84.0	18	2	AAR31905	Aar31905 Peptide b	
17	21	84.0	26	2	AAW54336	Aaw54336 Bradykini	
18	21	84.0	28	5	AAU90823	Aau90823 Insulin/i	
19	21	84.0	38	2	AAW42521	Aaw42521 Peptide d	
20	21	84.0	47	1	AAP80078	Aap80078 Cytomegal	

21	21	84.0	50	4	AAU63044	Aau63044	Propionib
22	21	84.0	50	6	ABM59563	Abm59563	Propionib
23	21	84.0	53	7	ADE86976	Ade86976	Human pan
24	21	84.0	60	4	AAU42979	Aau42979	Propionib
25	21	84.0	60	6	ABM39498	Abm39498	Propionib
26	21	84.0	61	4	AAU67822	Aau67822	Propionib
27	21	84.0	61	6	ABM64341	Abm64341	Propionib
28	21	84.0	63	3	AAB38568	Aab38568	Human sec
29	21	84.0	69	3	AAG47936	Aag47936	Arabidops
30	21	84.0	70	3	AAG09569	Aag09569	Arabidops
31	21	84.0	70	3	AAG47945	Aag47945	Arabidops
32	21	84.0	71	4	AAM65050	Aam65050	Human bra
33	21	84.0	71	5	ABG46788	Abg46788	Human pep
34	21	84.0	72	3	AAG23885	Aag23885	Arabidops
35	21	84.0	75	3	AAG24265	Aag24265	Arabidops
36	21	84.0	75	5	ABP33824	Abp33824	Human kin
37	21	84.0	85	4	AAU23614	Aau23614	Novel hum
38	21	84.0	85	4	AAU67726	Aau67726	Propionib
39	21	84.0	85	6	ABM64245	Abm64245	Propionib
40	21	84.0	92	4	AAM86518	Aam86518	Human imm
41	21	84.0	92	4	AAO10217	Aao10217	Human pol
42	21	84.0	92	4	ABG28498	Abg28498	Novel hum
43	21	84.0	95	3	AAB28004	Aab28004	Human sec
44	21	84.0	95	4	AAU64259	Aau64259	Propionib
45	21	84.0	95	4	AAU67642	Aau67642	Propionib

Title: US-09-929-924-9
Perfect score: 25
Sequence: 1 VVQVVA 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 264921

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	21	84.0	8	4	US-09-257-525A-2	Sequence 2, Appli
2	21	84.0	9	2	US-08-621-803-195	Sequence 195, App
3	21	84.0	9	3	US-09-217-352-195	Sequence 195, App
4	21	84.0	15	4	US-09-257-525A-3	Sequence 3, Appli
5	21	84.0	18	1	US-08-178-268-23	Sequence 23, Appl
6	21	84.0	26	3	US-08-676-242-15	Sequence 15, Appl
7	21	84.0	36	6	5231168-14	Patent No. 5231168
8	21	84.0	96	3	US-09-101-167-10	Sequence 10, Appl
9	21	84.0	97	3	US-08-818-112-72	Sequence 72, Appl
10	21	84.0	97	4	US-08-818-111-73	Sequence 73, Appl
11	21	84.0	97	4	US-09-056-556-72	Sequence 72, Appl
12	21	84.0	97	4	US-09-072-596-73	Sequence 73, Appl
13	21	84.0	97	4	US-09-072-967-72	Sequence 72, Appl
14	20	80.0	14	4	US-09-630-115-4	Sequence 4, Appli
15	20	80.0	18	1	US-08-178-268-25	Sequence 25, Appl
16	20	80.0	18	4	US-09-268-480-23	Sequence 23, Appl
17	20	80.0	32	3	US-08-433-522A-16	Sequence 16, Appl
18	20	80.0	32	3	US-09-135-166-16	Sequence 16, Appl
19	20	80.0	32	3	US-08-942-046-16	Sequence 16, Appl
20	20	80.0	49	4	US-09-450-072-72	Sequence 72, Appl
21	20	80.0	49	4	US-09-351-348-72	Sequence 72, Appl
22	20	80.0	52	4	US-09-904-615-99	Sequence 99, Appl

23	20	80.0	57	4	US-09-621-976-6261	Sequence 6261, Ap
24	20	80.0	66	2	US-08-162-081B-42	Sequence 42, Appl
25	20	80.0	66	2	US-08-780-872-42	Sequence 42, Appl
26	20	80.0	66	3	US-09-085-957-42	Sequence 42, Appl
27	20	80.0	70	4	US-09-621-976-6602	Sequence 6602, Ap
28	20	80.0	77	4	US-09-134-000C-4977	Sequence 4977, Ap
29	20	80.0	95	4	US-08-858-207A-516	Sequence 516, App
30	20	80.0	96	4	US-09-489-039A-10155	Sequence 10155, A
31	19	76.0	17	3	US-09-164-186-6	Sequence 6, Appli
32	19	76.0	17	3	US-09-164-186-15	Sequence 15, Appl
33	19	76.0	18	2	US-07-952-853-18	Sequence 18, Appl
34	19	76.0	18	2	US-08-914-848-18	Sequence 18, Appl
35	19	76.0	25	1	US-08-338-127-3	Sequence 3, Appli
36	19	76.0	25	4	US-09-101-307D-4	Sequence 4, Appli
37	19	76.0	25	4	US-09-665-362A-1	Sequence 1, Appli
38	19	76.0	33	3	US-09-164-186-9	Sequence 9, Appli
39	19	76.0	53	4	US-09-621-976-5891	Sequence 5891, Ap
40	19	76.0	57	4	US-08-630-915A-136	Sequence 136, App
41	19	76.0	57	4	US-08-630-915A-219	Sequence 219, App
42	19	76.0	58	4	US-09-275-252A-33	Sequence 33, Appl
43	19	76.0	62	4	US-08-630-915A-135	Sequence 135, App
44	19	76.0	66	1	US-08-208-008C-8	Sequence 8, Appli
45	19	76.0	70	4	US-09-489-039A-7312	Sequence 7312, Ap

Title: US-09-929-924-9
Perfect score: 25
Sequence: 1 VVQVVA 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1276540 seqs, 311283816 residues

Total number of hits satisfying chosen parameters: 533274

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
- 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	25	100.0	6	9	US-09-929-924-9	Sequence 9, Appli
2	25	100.0	6	9	US-09-929-924-19	Sequence 19, Appl
3	25	100.0	12	9	US-09-929-924-15	Sequence 15, Appl
4	25	100.0	67	12	US-10-424-599-216120	Sequence 216120,
5	25	100.0	72	9	US-09-929-924-17	Sequence 17, Appl
6	24	96.0	10	13	US-10-006-557-13	Sequence 13, Appl
7	24	96.0	78	12	US-10-424-599-250284	Sequence 250284,
8	22	88.0	48	12	US-10-424-599-241149	Sequence 241149,
9	22	88.0	54	12	US-10-424-599-221171	Sequence 221171,
10	22	88.0	63	12	US-10-424-599-241705	Sequence 241705,

11	22	88.0	66	16	US-10-437-963-131467	Sequence 131467,
12	22	88.0	71	16	US-10-437-963-145411	Sequence 145411,
13	22	88.0	96	16	US-10-437-963-179764	Sequence 179764,
14	22	88.0	98	16	US-10-437-963-188604	Sequence 188604,
15	21	84.0	8	9	US-09-935-682-2	Sequence 2, Appli
16	21	84.0	9	9	US-09-765-527-195	Sequence 195, App
17	21	84.0	16	9	US-09-935-682-3	Sequence 3, Appli
18	21	84.0	38	14	US-10-288-220-10	Sequence 10, Appl
19	21	84.0	41	12	US-10-424-599-150089	Sequence 150089,
20	21	84.0	51	12	US-10-424-599-225586	Sequence 225586,
21	21	84.0	59	12	US-10-424-599-263946	Sequence 263946,
22	21	84.0	62	12	US-10-424-599-156759	Sequence 156759,
23	21	84.0	67	12	US-10-424-599-175836	Sequence 175836,
24	21	84.0	69	16	US-10-437-963-190575	Sequence 190575,
25	21	84.0	71	9	US-09-864-761-46170	Sequence 46170, A
26	21	84.0	72	16	US-10-437-963-135855	Sequence 135855,
27	21	84.0	73	16	US-10-437-963-193513	Sequence 193513,
28	21	84.0	75	11	US-09-864-408A-5594	Sequence 5594, Ap
29	21	84.0	75	12	US-10-424-599-216247	Sequence 216247,
30	21	84.0	79	12	US-10-424-599-227753	Sequence 227753,
31	21	84.0	82	16	US-10-437-963-135317	Sequence 135317,
32	21	84.0	83	12	US-10-424-599-154454	Sequence 154454,
33	21	84.0	85	12	US-10-424-599-189626	Sequence 189626,
34	21	84.0	86	12	US-10-424-599-280528	Sequence 280528,
35	21	84.0	87	12	US-10-424-599-217639	Sequence 217639,
36	21	84.0	93	14	US-10-156-761-10196	Sequence 10196, A
37	21	84.0	94	16	US-10-437-963-115898	Sequence 115898,
38	21	84.0	97	14	US-10-193-002-73	Sequence 73, Appl
39	21	84.0	97	14	US-10-084-843-72	Sequence 72, Appl
40	21	84.0	97	16	US-10-437-963-160146	Sequence 160146,
41	21	84.0	98	16	US-10-437-963-145364	Sequence 145364,
42	21	84.0	99	12	US-10-424-599-189627	Sequence 189627,
43	20	80.0	16	10	US-09-788-051-14	Sequence 14, Appl
44	20	80.0	18	14	US-10-244-488-23	Sequence 23, Appl
45	20	80.0	21	10	US-09-974-879-273	Sequence 273, App

Title: US-09-929-924-9
Perfect score: 25
Sequence: 1 VVQVVA 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 37674

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Query	Match	Length	DB	ID	Description
No.		%					
1	22	88.0	53	2	H82739	hypothetical prote	
2	21	84.0	69	2	G69188	hypothetical prote	
3	21	84.0	75	2	E82859	hypothetical prote	
4	21	84.0	77	2	F90702	hypothetical prote	
5	21	84.0	77	2	A85553	hypothetical prote	
6	21	84.0	77	2	G64784	ybcJ protein - Esc	
7	21	84.0	82	2	I51180	gonadotropin-relea	
8	21	84.0	82	2	I51355	gonadotropin relea	
9	21	84.0	82	2	I51365	gonadotropin-relea	
10	21	84.0	82	2	I51331	gonadotropin relea	
11	21	84.0	87	2	I40094	hypothetical prote	
12	21	84.0	89	2	A82718	30S ribosomal prot	
13	21	84.0	93	2	T35660	probable acylphosp	
14	21	84.0	98	2	S62346	L71-5 protein - fr	
15	21	84.0	100	2	A97400	ysa protein [impor	
16	21	84.0	100	2	AB2618	integration host f	
17	20	80.0	36	2	B95156	hypothetical prote	
18	20	80.0	57	2	A39508	lipocortin IV - ra	
19	20	80.0	60	2	S51234	puc1A protein - Rh	
20	20	80.0	64	2	E82778	hypothetical prote	
21	20	80.0	64	2	AH0151	probable bacteriop	
22	20	80.0	71	2	A31332	Ca2+-transporting	
23	20	80.0	84	2	S59105	conserved hypothet	
24	20	80.0	85	2	A28561	late lactation pro	

25	20	80.0	85	2	G75315	hypothetical prote
26	20	80.0	96	2	AI3313	hypothetical prote
27	19	76.0	15	2	S70719	H ⁺ -transporting tw
28	19	76.0	36	2	A82208	hypothetical prote
29	19	76.0	53	2	G90776	hypothetical prote
30	19	76.0	53	2	D95878	conserved hypothet
31	19	76.0	55	2	G90765	hypothetical prote
32	19	76.0	55	2	T03337	gene e30 protein -
33	19	76.0	55	2	AC2366	hypothetical prote
34	19	76.0	58	2	E95124	conserved domain p
35	19	76.0	65	2	D83827	Na ⁺ /H ⁺ antiporter
36	19	76.0	66	2	D64403	hypothetical prote
37	19	76.0	66	2	AG3469	hypothetical prote
38	19	76.0	68	2	S66566	biotin carboxyl ca
39	19	76.0	69	2	A64961	outer membrane por
40	19	76.0	70	2	T17998	hypothetical prote
41	19	76.0	71	4	A58658	hypothetical colla
42	19	76.0	73	2	D64683	ribosomal protein
43	19	76.0	77	2	AI3031	hypothetical prote
44	19	76.0	77	2	B98254	hypothetical prote
45	19	76.0	79	2	AI2512	hypothetical prote

Title: US-09-929-924-9
 Perfect score: 25
 Sequence: 1 VVQVVA 6

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 15046

Minimum DB seq length: 0
 Maximum DB seq length: 100

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		%					Description
Result	Query	Match	Length	DB	ID		
No.	Score						
1	21	84.0	30	1	IHFB_RHILE	P80606	rhizobium l
2	21	84.0	70	1	R17E_METKA	Q8tuz3	methanopyru
3	21	84.0	70	1	YBCJ_ECOLI	P45571	escherichia
4	21	84.0	82	1	GON3_ONCMA	P30973	oncorhynchu
5	21	84.0	82	1	GON3_SALSA	P35629	salmo salar
6	21	84.0	82	1	GON3_SALTR	P45653	salmo trutt
7	21	84.0	100	1	IHFB_AGR5	Q8uif9	agrobacteri
8	20	80.0	84	1	DHSD_CHOCR	P54323	chondrus cr
9	20	80.0	94	1	IHFB_BRUME	Q8yet3	brucella me
10	20	80.0	94	1	IHFB_BRUSU	Q8g304	brucella su
11	20	80.0	94	1	IHFB_RHILO	Q98gs0	rhizobium l
12	19	76.0	52	1	YOAH_HAEIN	P56507	haemophilus
13	19	76.0	66	1	Y828_METJA	Q58238	methanococc
14	19	76.0	73	1	RL24_HELPY	P56049	helicobacte
15	19	76.0	89	1	CYB_BRANA	P49390	brassica na
16	18	72.0	22	1	CPI4_SOLTU	P58602	solanum tub
17	18	72.0	24	1	CR16_LITXA	P56231	litoria xan
18	18	72.0	24	1	CR18_LITCH	P81251	litoria chl
19	18	72.0	24	1	CR19_LITCH	P81252	litoria chl
20	18	72.0	25	1	CR11_LITSP	P56226	litoria spl
21	18	72.0	25	1	CR12_LITCE	P56227	litoria cae
22	18	72.0	25	1	CR13_LITCE	P56228	litoria cae
23	18	72.0	25	1	CR14_LITGI	P56229	litoria gil
24	18	72.0	25	1	CR15_LITCE	P56230	litoria cae
25	18	72.0	25	1	CR1A_LITSP	P82104	litoria spl
26	18	72.0	32	1	LPID_EDWTA	P08140	edwardsiell
27	18	72.0	38	1	RL7_VIBCO	P05395	vibrio cost
28	18	72.0	39	1	PSBJ_SYNP2	Q8rsw0	synechococc

29	18	72.0	39	1	PSBJ_SYNY3	P73070	synechocyst
30	18	72.0	48	1	LHB1_RHOTE	P80590	rhodocyclus
31	18	72.0	55	1	V6K_BYDVP	P09518	barley yell
32	18	72.0	65	1	ITR1_TRIKI	Q43667	trichosanth
33	18	72.0	69	1	YVCA_VACCC	P21119	vaccinia vi
34	18	72.0	74	1	PSAE_SYNP6	P23077	synechococc
35	18	72.0	75	1	SGS8_DROME	P02842	drosophila
36	18	72.0	76	1	AMC_RABIT	P82535	oryctolagus
37	18	72.0	79	1	YF90_MYCTU	O06600	mycobacteri
38	18	72.0	80	1	COXM_MOUSE	P56393	mus musculu
39	18	72.0	86	1	ACP_RICCN	Q92gd8	rickettsia
40	18	72.0	86	1	ACP_RICPR	Q9zch9	rickettsia
41	18	72.0	86	1	RS28_AERPE	Q9y9a6	aeropyrum p
42	18	72.0	87	1	YBED_ECOLI	P30977	escherichia
43	18	72.0	87	1	YBED_SALTY	Q8xgv6	salmonella
44	18	72.0	87	1	YQ00_YERPE	Q8zdg8	yersinia pe
45	18	72.0	90	1	GON3_ORYLA	Q9dd49	o progonado

Title: US-09-929-924-9
Perfect score: 25
Sequence: 1 VVQVVA 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 175362

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_25:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp Vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		%					
No.	Score	Query	Match	Length	DB	ID	Description
1	25	100.0	90	11	P70443	P70443	mus musculu
2	22	88.0	53	16	Q9PEQ7	Q9peq7	xylella fas
3	22	88.0	79	6	Q9GLJ3	Q9glj3	sus scrofa
4	22	88.0	89	16	Q8PBD3	Q8pbd3	xanthomonas
5	21	84.0	33	13	Q9W7G0	Q9w7g0	oncorhynchu
6	21	84.0	53	4	Q7Z493	Q7z493	homo sapien
7	21	84.0	54	13	Q90W09	Q90w09	oncorhynchu
8	21	84.0	60	13	Q8JHV5	Q8jhv5	heteralocha
9	21	84.0	68	16	Q8PEN3	Q8pen3	xanthomonas
10	21	84.0	69	5	O15559	O15559	trichomonas
11	21	84.0	69	17	O26763	O26763	methanobact

12	21	84.0	73	5	O15577	O15577 entamoeba h
13	21	84.0	75	16	Q9PHC2	Q9phc2 xylella fas
14	21	84.0	77	16	Q8XCT7	Q8xct7 escherichia
15	21	84.0	77	16	Q8FK42	Q8fk42 escherichia
16	21	84.0	77	16	Q833G1	Q833g1 enterococcu
17	21	84.0	78	16	Q7VGD3	Q7vgd3 helicobacte
18	21	84.0	82	9	Q8HAD8	Q8had8 salmonella
19	21	84.0	82	13	Q92094	Q92094 oncorhynchu
20	21	84.0	82	13	Q90VY3	Q90vy3 oncorhynchu
21	21	84.0	82	13	Q9I8P9	Q9i8p9 oncorhynchu
22	21	84.0	82	13	Q9I8Q0	Q9i8q0 oncorhynchu
23	21	84.0	82	16	Q9RD33	Q9rd33 streptomyce
24	21	84.0	83	9	Q853T7	Q853t7 mycobacteri
25	21	84.0	86	16	Q881E1	Q881e1 pseudomonas
26	21	84.0	87	2	Q44954	Q44954 bacillus br
27	21	84.0	88	10	Q9SE98	Q9se98 nicotiana t
28	21	84.0	89	16	Q9PE67	Q9pe67 xylella fas
29	21	84.0	89	16	Q87E73	Q87e73 xylella fas
30	21	84.0	92	5	Q8MTP2	Q8mtp2 bombyx mori
31	21	84.0	92	15	Q80345	Q80345 human immun
32	21	84.0	93	16	Q9ZBQ3	Q9zbq3 streptomyce
33	21	84.0	93	16	Q82JU5	Q82ju5 streptomyce
34	21	84.0	94	15	Q80349	Q80349 human immun
35	21	84.0	95	9	Q7Y293	Q7y293 phage phi 4
36	21	84.0	97	10	Q851N8	Q851n8 oryza sativ
37	21	84.0	98	5	Q24074	Q24074 drosophila
38	21	84.0	98	11	Q8BZB9	Q8bzb9 mus musculu
39	21	84.0	100	11	Q9D6T9	Q9d6t9 mus musculu
40	20	80.0	22	4	Q9UPC7	Q9upc7 homo sapien
41	20	80.0	22	11	Q9QX20	Q9qx20 mus musculu
42	20	80.0	36	16	Q97Q81	Q97q81 streptococc
43	20	80.0	45	2	Q50860	Q50860 myxococcus
44	20	80.0	49	16	Q8KEE8	Q8kee8 chlorobium
45	20	80.0	52	12	Q9DLS0	Q9dls0 mucosal dis

Title: US-09-929-924-11
 Perfect score: 26
 Sequence: 1 VVQKVA 6

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 891005

Minimum DB seq length: 0
 Maximum DB seq length: 100

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
 1: geneseqp1980s:*
 2: geneseqp1990s:*
 3: geneseqp2000s:*
 4: geneseqp2001s:*
 5: geneseqp2002s:*
 6: geneseqp2003as:*
 7: geneseqp2003bs:*
 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		%	Query				
No.	Score	Match	Length	DB	ID	Description	
1	26	100.0	6	4	AAB70013	Aab70013	Mammalian
2	23	88.5	14	4	AAM97713	Aam97713	Human pep
3	23	88.5	79	6	ABU29475	Abu29475	Protein e
4	23	88.5	89	7	ADC95418	Adc95418	E. faeciu
5	22	84.6	8	4	AAM23402	Aam23402	HIV pepti
6	22	84.6	8	4	AAM22441	Aam22441	HIV pepti
7	22	84.6	8	4	AAM22924	Aam22924	HIV pepti
8	22	84.6	8	4	AAM22861	Aam22861	HIV pepti
9	22	84.6	9	4	AAM22205	Aam22205	HIV pepti
10	22	84.6	9	4	AAM22197	Aam22197	HIV pepti
11	22	84.6	9	4	AAM23277	Aam23277	HIV pepti
12	22	84.6	9	4	AAM22198	Aam22198	HIV pepti
13	22	84.6	9	4	AAM22204	Aam22204	HIV pepti
14	22	84.6	9	6	ABR24779	Abr24779	Human can
15	22	84.6	9	6	ABR24987	Abr24987	Human can
16	22	84.6	10	6	ABR25073	Abr25073	Human can
17	22	84.6	10	6	ABR24534	Abr24534	Human can
18	22	84.6	10	6	ABR24874	Abr24874	Human can
19	22	84.6	10	6	ABR24887	Abr24887	Human can
20	22	84.6	10	6	ABR25156	Abr25156	Human can

21	22	84.6	10	6	ABR25702	Abr25702	Human can
22	22	84.6	15	6	AAO29814	Aao29814	hTRT MHC
23	22	84.6	15	6	AAO29815	Aao29815	hTRT MHC
24	22	84.6	42	4	AAM96104	Aam96104	Human rep
25	22	84.6	42	4	AAU22798	Aau22798	Human pro
26	22	84.6	46	4	AAO12491	Aao12491	Human pol
27	22	84.6	50	4	ABG02690	Abg02690	Novel hum
28	22	84.6	54	4	AAU63674	Aau63674	Propionib
29	22	84.6	54	6	ABM60193	Abm60193	Propionib
30	22	84.6	65	6	ABU58155	Abu58155	Corn stre
31	22	84.6	70	3	AAG33091	Aag33091	Zea mays
32	22	84.6	77	3	AAU65683	Aay65683	C. elegan
33	22	84.6	82	6	ABU58156	Abu58156	Corn stre
34	22	84.6	83	3	AAG01923	Aag01923	Human sec
35	21	80.8	8	4	ABP13199	Abp13199	HIV A02 s
36	21	80.8	9	4	AAM22203	Aam22203	HIV pepti
37	21	80.8	9	4	AAM22200	Aam22200	HIV pepti
38	21	80.8	9	4	ABP13409	Abp13409	HIV A02 s
39	21	80.8	9	4	ABP19096	Abp19096	HIV B62 s
40	21	80.8	9	4	ABP21398	Abp21398	HIV A03 m
41	21	80.8	9	4	ABP13408	Abp13408	HIV A02 s
42	21	80.8	10	4	ABP16160	Abp16160	HIV A24 s
43	21	80.8	10	4	ABP13639	Abp13639	HIV A02 s
44	21	80.8	10	4	ABP13641	Abp13641	HIV A02 s
45	21	80.8	10	4	ABP21401	Abp21401	HIV A03 m

Title: US-09-929-924-11
Perfect score: 26
Sequence: 1 VVQKVA 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 264921

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	23	88.5	89	4	US-09-107-532A-5045	Sequence 5045, Ap
2	22	84.6	50	4	US-09-621-976-6430	Sequence 6430, Ap
3	22	84.6	77	4	US-09-084-303B-206	Sequence 206, Appl
4	22	84.6	78	2	US-08-469-412A-13	Sequence 13, Appl
5	22	84.6	78	3	US-09-021-715-13	Sequence 13, Appl
6	22	84.6	82	4	US-09-252-991A-23597	Sequence 23597, A
7	22	84.6	88	4	US-09-621-976-7095	Sequence 7095, Ap
8	21	80.8	13	3	US-08-834-314-5	Sequence 5, Appli
9	21	80.8	85	4	US-09-540-236-2516	Sequence 2516, Ap
10	21	80.8	86	4	US-08-858-207A-471	Sequence 471, App
11	21	80.8	88	4	US-09-732-210-193	Sequence 193, App
12	21	80.8	97	4	US-09-540-236-2768	Sequence 2768, Ap
13	20	76.9	11	2	US-08-436-420-21	Sequence 21, Appl
14	20	76.9	12	2	US-08-436-420-23	Sequence 23, Appl
15	20	76.9	13	3	US-08-159-339A-1118	Sequence 1118, Ap
16	20	76.9	19	2	US-08-436-420-13	Sequence 13, Appl
17	20	76.9	19	2	US-08-436-420-24	Sequence 24, Appl
18	20	76.9	22	1	US-07-778-413E-2	Sequence 2, Appli
19	20	76.9	22	1	US-08-340-102-2	Sequence 2, Appli
20	20	76.9	23	3	US-08-746-160-34	Sequence 34, Appl
21	20	76.9	23	3	US-08-810-324-30	Sequence 30, Appl
22	20	76.9	40	2	US-08-807-332B-32	Sequence 32, Appl

23	20	76.9	40	3	US-09-338-876-32	Sequence 32, Appl
24	20	76.9	50	1	US-08-321-071A-29	Sequence 29, Appl
25	20	76.9	61	4	US-09-134-000C-3506	Sequence 3506, Ap
26	20	76.9	63	4	US-09-107-532A-4494	Sequence 4494, Ap
27	20	76.9	63	4	US-09-540-236-2384	Sequence 2384, Ap
28	20	76.9	64	4	US-09-540-236-2424	Sequence 2424, Ap
29	20	76.9	65	4	US-09-177-304-4	Sequence 4, Appli
30	20	76.9	67	4	US-09-540-236-2191	Sequence 2191, Ap
31	20	76.9	70	4	US-09-252-991A-19377	Sequence 19377, A
32	20	76.9	75	2	US-08-436-420-14	Sequence 14, Appl
33	20	76.9	75	2	US-08-436-420-15	Sequence 15, Appl
34	20	76.9	75	2	US-08-468-819-12	Sequence 12, Appl
35	20	76.9	75	4	US-09-213-383-12	Sequence 12, Appl
36	20	76.9	77	4	US-09-543-681A-7744	Sequence 7744, Ap
37	20	76.9	78	1	US-07-778-413E-12	Sequence 12, Appl
38	20	76.9	78	1	US-08-340-102-12	Sequence 12, Appl
39	20	76.9	78	1	US-08-330-163-8	Sequence 8, Appli
40	20	76.9	78	1	US-08-482-111-8	Sequence 8, Appli
41	20	76.9	78	2	US-08-436-420-32	Sequence 32, Appl
42	20	76.9	79	2	US-08-117-952-750	Sequence 750, App
43	20	76.9	82	4	US-09-446-920-2	Sequence 2, Appli
44	20	76.9	99	4	US-09-621-976-4603	Sequence 4603, Ap
45	19	73.1	11	6	5210075-10	Patent No. 5210075

Sequence: 1 VVQKVA 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1276540 seqs, 311283816 residues

Total number of hits satisfying chosen parameters: 533274

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
- 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	26	100.0	6	9	US-09-929-924-11	Sequence 11, Appl
2	23	88.5	39	16	US-10-437-963-185063	Sequence 185063,
3	23	88.5	41	16	US-10-437-963-129086	Sequence 129086,
4	23	88.5	77	12	US-10-424-599-157757	Sequence 157757,
5	23	88.5	79	12	US-10-282-122A-57399	Sequence 57399, A
6	22	84.6	8	12	US-10-182-252A-326	Sequence 326, App
7	22	84.6	8	12	US-10-182-252A-746	Sequence 746, App
8	22	84.6	8	12	US-10-182-252A-809	Sequence 809, App
9	22	84.6	8	12	US-10-182-252A-1287	Sequence 1287, Ap
10	22	84.6	9	12	US-10-182-252A-82	Sequence 82, Appl
11	22	84.6	9	12	US-10-182-252A-83	Sequence 83, Appl
12	22	84.6	9	12	US-10-182-252A-89	Sequence 89, Appl

13	22	84.6	9	12	US-10-182-252A-90	Sequence 90, Appl
14	22	84.6	9	12	US-10-182-252A-1162	Sequence 1162, Ap
15	22	84.6	15	14	US-10-282-960-55	Sequence 55, Appl
16	22	84.6	15	14	US-10-282-960-56	Sequence 56, Appl
17	22	84.6	42	10	US-09-764-891-4762	Sequence 4762, Ap
18	22	84.6	42	14	US-10-091-572-317	Sequence 317, App
19	22	84.6	55	12	US-10-424-599-193678	Sequence 193678,
20	22	84.6	65	13	US-10-078-929-16	Sequence 16, Appl
21	22	84.6	70	12	US-10-424-599-154204	Sequence 154204,
22	22	84.6	70	12	US-10-424-599-167496	Sequence 167496,
23	22	84.6	70	12	US-10-424-599-204061	Sequence 204061,
24	22	84.6	70	16	US-10-437-963-171085	Sequence 171085,
25	22	84.6	71	12	US-10-424-599-214155	Sequence 214155,
26	22	84.6	71	16	US-10-437-963-129578	Sequence 129578,
27	22	84.6	76	12	US-10-424-599-267422	Sequence 267422,
28	22	84.6	76	16	US-10-437-963-187944	Sequence 187944,
29	22	84.6	77	14	US-10-339-740-206	Sequence 206, App
30	22	84.6	78	16	US-10-437-963-130909	Sequence 130909,
31	22	84.6	79	12	US-10-424-599-219575	Sequence 219575,
32	22	84.6	80	16	US-10-437-963-203117	Sequence 203117,
33	22	84.6	82	13	US-10-078-929-18	Sequence 18, Appl
34	22	84.6	88	12	US-10-424-599-188761	Sequence 188761,
35	22	84.6	88	12	US-10-424-599-242836	Sequence 242836,
36	22	84.6	89	16	US-10-437-963-118933	Sequence 118933,
37	22	84.6	90	16	US-10-437-963-112481	Sequence 112481,
38	22	84.6	96	12	US-10-424-599-178624	Sequence 178624,
39	22	84.6	98	16	US-10-437-963-141860	Sequence 141860,
40	22	84.6	100	12	US-10-424-599-228933	Sequence 228933,
41	21	80.8	9	12	US-10-182-252A-85	Sequence 85, Appl
42	21	80.8	9	12	US-10-182-252A-88	Sequence 88, Appl
43	21	80.8	52	12	US-10-424-599-279462	Sequence 279462,
44	21	80.8	55	12	US-10-424-599-199051	Sequence 199051,
45	21	80.8	56	12	US-10-424-599-232620	Sequence 232620,

Title: US-09-929-924-11
 Perfect score: 26
 Sequence: 1 VVQKVA 6

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 37674

Minimum DB seq length: 0
 Maximum DB seq length: 100

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : PIR_78:*
 1: pir1:*
 2: pir2:*
 3: pir3:*
 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	24	92.3	42	2	A36533	H+-transporting tw
2	23	88.5	86	2	T31846	hypothetical prote
3	22	84.6	19	2	S32675	nitrogen fixation
4	22	84.6	60	2	S43777	hypothetical prote
5	22	84.6	68	2	B88596	protein T28D6.6 [i
6	22	84.6	69	2	F95914	hypothetical prote
7	22	84.6	83	2	E84142	hypothetical prote
8	21	80.8	64	1	WMIHB2	3b protein - avian
9	21	80.8	64	1	WMIHB5	3b protein - avian
10	21	80.8	68	2	D90507	hypothetical prote
11	21	80.8	76	2	G84535	hypothetical prote
12	21	80.8	87	2	S50134	nitrogen fixation
13	21	80.8	88	2	T43379	40s ribosomal prot
14	21	80.8	88	2	A46411	conserved hypothet
15	21	80.8	89	2	T50250	40s ribosomal prot
16	21	80.8	91	2	A69518	glutaredoxin (grx-
17	20	76.9	51	2	I51028	paired box transcr
18	20	76.9	66	2	H98064	hypothetical prote
19	20	76.9	71	2	G75418	hypothetical prote
20	20	76.9	73	2	JQ1921	hypothetical 8.5K
21	20	76.9	73	2	H82772	hypothetical prote
22	20	76.9	74	2	S77212	hypothetical prote
23	20	76.9	75	2	B54188	granulocyte chemot
24	20	76.9	75	2	A54188	granulocyte chemot

25	20	76.9	78	2	T18084	hypothetical prote
26	20	76.9	78	2	AD3307	hypothetical prote
27	20	76.9	81	2	H85690	probable tail comp
28	20	76.9	82	2	S68162	SBH1 protein - yea
29	20	76.9	83	2	AD0081	hypothetical prote
30	20	76.9	91	2	D71713	hypothetical prote
31	20	76.9	99	2	PC4431	isoform 1 - bovine
32	20	76.9	100	2	S21467	macrophage inflamm
33	20	76.9	100	2	I55614	macrophage inflamm
34	19	73.1	16	2	S65709	major allergen Myr
35	19	73.1	53	1	RGBPA2	regulatory protein
36	19	73.1	55	2	I50177	alpha-1 type-3 col
37	19	73.1	63	2	B84092	hypothetical prote
38	19	73.1	63	2	AF1126	hypothetical prote
39	19	73.1	67	2	PC1239	focal adhesion kin
40	19	73.1	67	2	A72347	hypothetical prote
41	19	73.1	67	2	T01958	hypothetical prote
42	19	73.1	69	2	G69188	hypothetical prote
43	19	73.1	70	2	AF1967	hypothetical prote
44	19	73.1	71	2	E98138	hypothetical prote
45	19	73.1	75	2	E90974	probable cell divi

Title: US-09-929-924-11
Perfect score: 26
Sequence: 1 VVQKVA 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 15046

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	% Query Match	Length	DB	ID	Description
1	21	80.8	16	1	CT11_LITCI	P81835 litoria cit
2	21	80.8	18	1	CT1A_LITCI	P81838 litoria cit
3	21	80.8	18	1	CT1B_LITCI	P81839 litoria cit
4	21	80.8	64	1	V3B_IBVB	P30241 avian infec
5	21	80.8	64	1	V3B_IBVM	P05138 avian infec
6	21	80.8	81	1	TRUA_SYNP6	O24712 synechococc
7	21	80.8	88	1	R25Z_SCHPO	O74172 schizosacch
8	21	80.8	88	1	YIHD_HAEIN	P44900 haemophilus
9	21	80.8	88	1	YJ28_PASMU	Q9cjr4 pasteurella
10	21	80.8	89	1	R25Y_SCHPO	P79009 schizosacch
11	21	80.8	91	1	THIO_ARCFU	O28137 archaeoglob
12	21	80.8	93	1	IHFB_RHOSH	Q9x4e2 rhodobacter
13	20	76.9	16	1	CT12_LITCI	P81840 litoria cit
14	20	76.9	16	1	CT13_LITCI	P81846 litoria cit
15	20	76.9	17	1	AU31_LITRA	P82394 litoria ran
16	20	76.9	17	1	AU32_LITRA	P82395 litoria ran
17	20	76.9	17	1	AU33_LITRA	P82396 litoria ran
18	20	76.9	18	1	CT1C_LITCI	P81844 litoria cit
19	20	76.9	18	1	CT1D_LITCI	P81845 litoria cit
20	20	76.9	57	1	GNSA_ECOLI	P52635 escherichia
21	20	76.9	73	1	YPO4_NPVLD	P30326 lymantria d
22	20	76.9	82	1	S6B1_YEAST	P52870 saccharomyc
23	20	76.9	91	1	Y052_RICPR	Q9ze93 rickettsia
24	20	76.9	94	1	VAP2_RIEAN	O85171 riemerella
25	20	76.9	100	1	MIP2_RAT	P30348 rattus norv
26	19	73.1	13	1	AU11_LITRA	P82386 litoria ran
27	19	73.1	13	1	AU12_LITRA	P82387 litoria ran
28	19	73.1	42	1	RL5_PROVU	P20031 proteus vul

29	19	73.1	53	1	RARC_BPP22	P03050	bacteriopha
30	19	73.1	60	1	RL30_THETH	P74909	thermus the
31	19	73.1	62	1	4OT4_PSEPU	Q93jw0	pseudomonas
32	19	73.1	77	1	NXP4_MACMU	Q8wmj7	macaca mula
33	19	73.1	80	1	DLC2_LACPL	Q88x40	lactobacill
34	19	73.1	81	1	ACP_GUIITH	P29189	guillardia
35	19	73.1	83	1	TMOB_PSEME	Q00457	pseudomonas
36	19	73.1	84	1	COAB_BPI22	P15416	bacteriopha
37	19	73.1	85	1	THIO_METJA	Q57755	methanococc
38	19	73.1	88	1	YB63_SHEON	Q8ehq4	shewanella
39	19	73.1	90	1	RS15_AQUAE	O66594	aquifex aeo
40	19	73.1	90	1	YMZB_BACSU	O31786	bacillus su
41	19	73.1	93	1	UBIL_NPVOP	Q05120	orgyia pseu
42	19	73.1	97	1	GATC_LISIN	Q92aq2	listeria in
43	19	73.1	97	1	GATC_LISMO	P58817	listeria mo
44	19	73.1	97	1	H1C2_TRYCR	P40268	trypanosoma
45	19	73.1	99	1	FLGM_PROMI	P96974	proteus mir

Title: US-09-929-924-11
Perfect score: 26
Sequence: 1 VVQKVA 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 175362

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_25:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp Vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result						Description
	No.	Score	% Match	Length	ID	
	1	23	88.5	68	12 O56878	O56878 gallid herp
	2	23	88.5	79	16 Q82ZE9	Q82ze9 enterococcu
	3	23	88.5	86	5 O16429	O16429 caenorhabdi
	4	23	88.5	90	9 Q856K8	Q856k8 mycobacteri
	5	22	84.6	19	2 Q44506	Q44506 anabaena va
	6	22	84.6	43	15 O92795	O92795 human immun
	7	22	84.6	43	15 O92796	O92796 human immun
	8	22	84.6	43	15 O92794	O92794 human immun
	9	22	84.6	43	15 O56200	O56200 human immun
	10	22	84.6	43	15 O92797	O92797 human immun
	11	22	84.6	43	15 O92798	O92798 human immun

12	22	84.6	60	2	Q08090	Q08090 synechococc
13	22	84.6	68	16	Q8CKN0	Q8ckn0 yersinia pe
14	22	84.6	69	16	Q92VW5	Q92vw5 rhizobium m
15	22	84.6	77	3	Q8TGT4	Q8tgt4 saccharomyc
16	22	84.6	83	16	Q9K5Z4	Q9k5z4 bacillus ha
17	22	84.6	84	2	Q8GPA3	Q8gpa3 streptococc
18	22	84.6	84	12	Q80HS6	Q80hs6 white spot
19	22	84.6	98	15	Q97759	Q97759 human immun
20	22	84.6	98	15	Q76964	Q76964 human immun
21	21	80.8	20	6	Q9TRB9	Q9trb9 bos taurus
22	21	80.8	43	15	O56207	O56207 human immun
23	21	80.8	43	15	Q9W968	Q9w968 human immun
24	21	80.8	43	15	O56206	O56206 human immun
25	21	80.8	48	2	Q9RAN8	Q9ran8 mesorhizobi
26	21	80.8	60	9	Q9MCI6	Q9mci6 bacteriopha
27	21	80.8	60	16	Q81EP8	Q81ep8 bacillus ce
28	21	80.8	62	2	Q9R5H7	Q9r5h7 aphanizomen
29	21	80.8	64	12	Q9J4A8	Q9j4a8 avian infec
30	21	80.8	68	17	Q97U08	Q97u08 sulfolobus
31	21	80.8	69	12	Q8QN31	Q8qn31 cowpox viru
32	21	80.8	73	16	Q8P2H4	Q8p2h4 streptococc
33	21	80.8	76	10	Q9XII5	Q9xii5 arabidopsis
34	21	80.8	79	3	Q7Z881	Q7z881 talaromyces
35	21	80.8	80	16	Q8CU43	Q8cu43 staphylococ
36	21	80.8	85	9	Q9AZA6	Q9aza6 lactobacill
37	21	80.8	86	5	Q26871	Q26871 trypanosoma
38	21	80.8	87	2	Q51295	Q51295 nostoc sp.
39	21	80.8	88	16	Q9CK35	Q9ck35 pasteurella
40	21	80.8	90	11	P70443	P70443 mus musculu
41	21	80.8	91	16	Q7VF12	Q7vf12 helicobacte
42	21	80.8	100	5	Q9BMD9	Q9bmd9 oxytricha t
43	20	76.9	17	8	Q9T2S0	Q9t2s0 solanum tub
44	20	76.9	30	12	Q84734	Q84734 phocine her
45	20	76.9	49	16	Q8FZB4	Q8fzb4 brucella su

Title: US-09-929-924-13
 Perfect score: 48
 Sequence: 1 GMWQCLLS 8

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 891005

Minimum DB seq length: 0
 Maximum DB seq length: 100

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
 1: geneseqp1980s:*
 2: geneseqp1990s:*
 3: geneseqp2000s:*
 4: geneseqp2001s:*
 5: geneseqp2002s:*
 6: geneseqp2003as:*
 7: geneseqp2003bs:*
 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	48	100.0	8	4	AAB70015	Aab70015 Mammalian
2	48	100.0	16	4	AAB70014	Aab70014 Mammalian
3	48	100.0	21	4	AAB89248	Aab89248 HIV gp120
4	48	100.0	21	4	AAB89247	Aab89247 HIV gp120
5	48	100.0	21	4	AAB89249	Aab89249 HIV gp120
6	48	100.0	73	4	AAB70018	Aab70018 Mammalian
7	46	95.8	73	4	AAB70029	Aab70029 Human CD4
8	46	95.8	73	4	AAB70028	Aab70028 Human CD4
9	45	93.8	12	4	AAB70016	Aab70016 Mammalian
10	45	93.8	72	4	AAB70019	Aab70019 Mammalian
11	43	89.6	73	4	AAB70025	Aab70025 Human CD4
12	42	87.5	73	4	AAB70026	Aab70026 Human CD4
13	42	87.5	73	4	AAB70027	Aab70027 Human CD4
14	40	83.3	21	4	AAB89246	Aab89246 HIV gp120
15	37	77.1	6	4	AAB70006	Aab70006 Mammalian
16	36	75.0	16	6	ABP82724	Abp82724 G protein
17	35	72.9	20	4	ABB44940	Abb44940 Rabbit al
18	35	72.9	24	2	AAY12811	Aay12811 Human 5'
19	35	72.9	31	4	AAM37243	Aam37243 Peptide #
20	35	72.9	53	6	ABP99903	Abp99903 Breast sp

21	35	72.9	63	4	AAG75143	Aag75143	Human col
22	35	72.9	66	3	AAG01769	Aag01769	Human sec
23	35	72.9	73	6	ABP78118	Abp78118	N. gonorr
24	35	72.9	77	5	ABP11011	Abp11011	Human ORF
25	34	70.8	25	5	ABG77058	Abg77058	Prostate
26	34	70.8	62	4	AAM95903	Aam95903	Human rep
27	34	70.8	62	4	ABB96434	Abb96434	Human tes
28	33	68.8	29	4	ABB37745	Abb37745	Peptide #
29	33	68.8	50	4	AAM96216	Aam96216	Human rep
30	33	68.8	50	4	ABB10893	Abb10893	Human ova
31	32	66.7	8	2	AAR35966	Aar35966	Hepatitis
32	32	66.7	8	2	AAR35967	Aar35967	Hepatitis
33	32	66.7	8	2	AAR35965	Aar35965	Hepatitis
34	32	66.7	9	4	AAU26981	Aau26981	Human Leu
35	32	66.7	9	4	AAU26648	Aau26648	Human Leu
36	32	66.7	16	3	AAB09223	Aab09223	Hepatitis
37	32	66.7	21	2	AAR33572	Aar33572	HCV fragm
38	32	66.7	21	4	AAB69030	Aab69030	HCV recom
39	32	66.7	22	2	AAY12625	Aay12625	Human 5'
40	32	66.7	25	4	AAM21523	Aam21523	Peptide #
41	32	66.7	25	4	ABB43868	Abb43868	Peptide #
42	32	66.7	25	4	AAM37783	Aam37783	Peptide #
43	32	66.7	25	4	ABB26794	Abb26794	Protein #
44	32	66.7	25	4	AAM77595	Aam77595	Human bon
45	32	66.7	25	4	AAM64852	Aam64852	Human bra

Title: US-09-929-924-13
 Perfect score: 48
 Sequence: 1 GMWQCLLS 8

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 264921

Minimum DB seq length: 0
 Maximum DB seq length: 100

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Issued_Patents_AA:*
 1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
 2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
 3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
 4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
 5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
 6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	48	100.0	83	2	US-08-332-562A-87	Sequence 87, Appl
2	32	66.7	8	3	US-08-444-818-449	Sequence 449, App
3	32	66.7	8	3	US-08-444-818-450	Sequence 450, App
4	32	66.7	8	3	US-08-444-818-451	Sequence 451, App
5	32	66.7	16	4	US-08-469-260A-345	Sequence 345, App
6	32	66.7	16	4	US-08-488-446-345	Sequence 345, App
7	32	66.7	16	4	US-08-467-344A-345	Sequence 345, App
8	32	66.7	21	3	US-08-867-611-55	Sequence 55, Appl
9	32	66.7	21	4	US-09-690-359-55	Sequence 55, Appl
10	32	66.7	87	2	US-08-477-451-45	Sequence 45, Appl
11	30	62.5	8	3	US-08-444-818-448	Sequence 448, App
12	30	62.5	30	4	US-08-857-636-67	Sequence 67, Appl
13	30	62.5	91	4	US-09-543-681A-8118	Sequence 8118, Ap
14	30	62.5	100	4	US-09-025-596-80	Sequence 80, Appl
15	30	62.5	100	4	US-09-073-661-80	Sequence 80, Appl
16	30	62.5	100	4	US-10-100-785-80	Sequence 80, Appl
17	29	60.4	10	2	US-08-406-330-16	Sequence 16, Appl
18	29	60.4	10	2	US-08-556-597-16	Sequence 16, Appl
19	29	60.4	14	2	US-08-449-933-11	Sequence 11, Appl
20	29	60.4	14	3	US-07-966-049A-11	Sequence 11, Appl
21	29	60.4	24	1	US-08-484-635-111	Sequence 111, App
22	29	60.4	24	2	US-08-484-631-111	Sequence 111, App

23	29	60.4	24	2	US-08-827-570-111	Sequence 111, App
24	29	60.4	26	4	US-08-817-441-56	Sequence 56, Appl
25	29	60.4	37	4	US-08-817-441-80	Sequence 80, Appl
26	29	60.4	44	4	US-09-369-247-94	Sequence 94, Appl
27	29	60.4	52	4	US-09-404-641-79	Sequence 79, Appl
28	29	60.4	56	4	US-09-621-976-6025	Sequence 6025, Ap
29	29	60.4	63	1	US-08-194-338-14	Sequence 14, Appl
30	29	60.4	77	4	US-09-621-976-5778	Sequence 5778, Ap
31	29	60.4	89	4	US-09-536-977-58	Sequence 58, Appl
32	29	60.4	98	2	US-08-248-839C-131	Sequence 131, App
33	28	58.3	11	3	US-09-224-785-8	Sequence 8, Appli
34	28	58.3	11	4	US-09-756-594-8	Sequence 8, Appli
35	28	58.3	12	3	US-08-776-949-30	Sequence 30, Appl
36	28	58.3	26	3	US-09-224-785-38	Sequence 38, Appl
37	28	58.3	26	4	US-09-756-594-38	Sequence 38, Appl
38	28	58.3	32	4	US-09-698-286A-35	Sequence 35, Appl
39	28	58.3	46	4	US-09-418-710-47	Sequence 47, Appl
40	28	58.3	46	4	US-09-418-710-60	Sequence 60, Appl
41	28	58.3	54	4	US-09-205-258-280	Sequence 280, App
42	28	58.3	68	4	US-09-312-283C-376	Sequence 376, App
43	28	58.3	81	2	US-08-332-562A-86	Sequence 86, Appl
44	28	58.3	81	4	US-09-252-991A-24724	Sequence 24724, A
45	28	58.3	85	4	US-09-732-210-42	Sequence 42, Appl

Title: US-09-929-924-13
Perfect score: 48
Sequence: 1 GMWQCLLS 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1276540 seqs, 311283816 residues

Total number of hits satisfying chosen parameters: 533274

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
- 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	48	100.0	8	9	US-09-929-924-13	Sequence 13, Appl
2	48	100.0	16	9	US-09-929-924-12	Sequence 12, Appl
3	48	100.0	21	14	US-10-084-813-354	Sequence 354, App
4	48	100.0	21	14	US-10-084-813-355	Sequence 355, App
5	48	100.0	21	14	US-10-084-813-356	Sequence 356, App
6	48	100.0	73	9	US-09-929-924-16	Sequence 16, Appl
7	46	95.8	73	9	US-09-929-924-36	Sequence 36, Appl
8	46	95.8	73	9	US-09-929-924-37	Sequence 37, Appl
9	45	93.8	12	9	US-09-929-924-14	Sequence 14, Appl
10	45	93.8	72	9	US-09-929-924-17	Sequence 17, Appl

11	43	89.6	73	9	US-09-929-924-33	Sequence 33, Appl
12	42	87.5	73	9	US-09-929-924-34	Sequence 34, Appl
13	42	87.5	73	9	US-09-929-924-35	Sequence 35, Appl
14	40	83.3	21	14	US-10-084-813-353	Sequence 353, App
15	38	79.2	83	9	US-09-771-161A-108	Sequence 108, App
16	37	77.1	6	9	US-09-929-924-4	Sequence 4, Appli
17	36	75.0	16	14	US-10-225-567A-1397	Sequence 1397, Ap
18	35	72.9	20	15	US-10-186-229-28	Sequence 28, Appl
19	35	72.9	31	9	US-09-864-761-48807	Sequence 48807, A
20	35	72.9	53	14	US-10-082-828A-184	Sequence 184, App
21	35	72.9	54	12	US-10-424-599-223359	Sequence 223359,
22	35	72.9	62	12	US-10-424-599-171255	Sequence 171255,
23	35	72.9	63	14	US-10-106-698-5917	Sequence 5917, Ap
24	34	70.8	25	14	US-10-000-256A-164	Sequence 164, App
25	34	70.8	49	14	US-10-029-386-31033	Sequence 31033, A
26	34	70.8	62	10	US-09-764-891-4561	Sequence 4561, Ap
27	34	70.8	64	12	US-10-424-599-212323	Sequence 212323,
28	34	70.8	75	12	US-10-424-599-229210	Sequence 229210,
29	33	68.8	29	9	US-09-864-761-47753	Sequence 47753, A
30	33	68.8	40	14	US-10-029-386-28338	Sequence 28338, A
31	33	68.8	50	10	US-09-764-891-4874	Sequence 4874, Ap
32	33	68.8	50	14	US-10-205-428-399	Sequence 399, App
33	33	68.8	51	14	US-10-029-386-29257	Sequence 29257, A
34	33	68.8	51	14	US-10-029-386-31895	Sequence 31895, A
35	33	68.8	62	12	US-10-424-599-246412	Sequence 246412,
36	33	68.8	63	14	US-10-029-386-31045	Sequence 31045, A
37	33	68.8	71	16	US-10-437-963-120376	Sequence 120376,
38	33	68.8	74	12	US-10-424-599-195133	Sequence 195133,
39	33	68.8	76	16	US-10-437-963-143360	Sequence 143360,
40	33	68.8	78	12	US-10-424-599-240007	Sequence 240007,
41	33	68.8	80	14	US-10-029-386-29168	Sequence 29168, A
42	33	68.8	83	16	US-10-437-963-132784	Sequence 132784,
43	33	68.8	92	12	US-10-424-599-206639	Sequence 206639,
44	33	68.8	96	12	US-10-424-599-152706	Sequence 152706,
45	32	66.7	16	8	US-08-424-550B-345	Sequence 345, App

Title: US-09-929-924-13
 Perfect score: 48
 Sequence: 1 GMWQCLLS 8

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 37674

Minimum DB seq length: 0
 Maximum DB seq length: 100

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : PIR_78:*
 1: pir1:*
 2: pir2:*
 3: pir3:*
 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	32	66.7	83	2	E75218	ribosomal protein
2	32	66.7	86	2	B71204	ribosomal protein
3	31	64.6	57	2	PQ0401	genome polyprotein
4	31	64.6	79	2	S24379	hypothetical prote
5	31	64.6	82	2	S74971	transposase ssr269
6	31	64.6	98	2	T18099	hypothetical prote
7	31	64.6	100	2	S76444	transposase slr016
8	31	64.6	100	2	S76090	transposase sll016
9	30	62.5	38	2	I70014	kallikrein - mouse
10	30	62.5	60	2	B82733	hypothetical prote
11	30	62.5	77	2	AE2043	hypothetical prote
12	30	62.5	91	1	MNVUAV	nonstructural prot
13	29	60.4	30	2	I52254	gene CYP11B2 prote
14	29	60.4	33	2	B58512	bromosleeper pepti
15	29	60.4	38	2	I70022	kallikrein - mouse
16	29	60.4	62	2	S25999	hypothetical prote
17	29	60.4	62	2	S22564	finger protein - h
18	29	60.4	73	2	AE3264	hypothetical prote
19	29	60.4	83	2	A69257	ribosomal protein
20	29	60.4	97	2	F82416	hypothetical prote
21	28	58.3	26	2	I45087	cysteine proteinas
22	28	58.3	57	2	S30502	protein-tyrosine k
23	28	58.3	57	2	E82667	hypothetical prote
24	28	58.3	87	2	C85825	hypothetical prote

25	28	58.3	87	2	F90979	hypothetical prote
26	28	58.3	87	2	T18182	hypothetical prote
27	28	58.3	89	2	G69190	ribosomal protein
28	28	58.3	91	2	JE0321	ribosomal protein
29	28	58.3	94	2	T40691	ribosomal protein
30	28	58.3	94	2	AG2364	hypothetical prote
31	28	58.3	96	2	C71614	ribosomal protein
32	28	58.3	96	2	T05760	hypothetical prote
33	27	56.2	42	2	I55360	ornithine-oxo-acid
34	27	56.2	55	2	H82976	rubredoxin PA5350
35	27	56.2	55	2	A82977	rubredoxin PA5351
36	27	56.2	64	2	D95331	conserved hypothet
37	27	56.2	71	2	I70114	arrestin-D - rat (
38	27	56.2	82	2	D84387	hypothetical prote
39	27	56.2	86	2	D72623	ribosomal protein
40	27	56.2	88	2	H91290	hypothetical prote
41	27	56.2	91	2	T26996	ribosomal protein
42	27	56.2	91	2	C90116	60S ribosomal prot
43	27	56.2	92	1	R5RT37	ribosomal protein
44	27	56.2	92	2	S42109	ribosomal protein
45	27	56.2	92	2	JN0875	ribosomal protein

Title: US-09-929-924-13
 Perfect score: 48
 Sequence: 1 GMWQCLLS 8

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 15046

Minimum DB seq length: 0
 Maximum DB seq length: 100

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		%					
Result		Query					
No.	Score	Match	Length	DB	ID	Description	
1	32	66.7	80	1	R37A_THEAC	Q9hip0 thermoplasm	
2	32	66.7	83	1	R37A_PYRAB	Q9v202 pyrococcus	
3	32	66.7	83	1	R37A_PYRFU	Q8tzi4 pyrococcus	
4	32	66.7	83	1	R37A_PYRHO	O74106 pyrococcus	
5	32	66.7	95	1	R37A_HALN1	Q9hsg8 halobacteri	
6	30	62.5	91	1	VNST_AINOV	P12413 aino virus.	
7	29	60.4	33	1	CXBW_CONRA	P58804 conus radia	
8	29	60.4	62	1	YM32_MARPO	P38474 marchantia	
9	29	60.4	83	1	R37A_ARCFU	O30179 archaeoglob	
10	29	60.4	91	1	R37A_SCHMA	O17307 schistosoma	
11	28	58.3	89	1	R37A_METKA	Q8tyc3 methanopyru	
12	28	58.3	89	1	R37A_METTH	O26777 methanobact	
13	28	58.3	94	1	RL43_SCHPO	O94686 schizosacch	
14	28	58.3	96	1	R37A_PLAFA	O96184 plasmodium	
15	27	56.2	17	1	CXMA_CONPE	P58926 conus penna	
16	27	56.2	71	1	ARRD_RAT	P36577 rattus norv	
17	27	56.2	72	1	DMS5_AGAAN	O93225 agalychnis	
18	27	56.2	85	1	R37A_MYXGL	Q9y0h7 myxine glut	
19	27	56.2	86	1	R37A_AERPE	Q9yc06 aeropyrum p	
20	27	56.2	90	1	R37A_OSTOS	O61598 ostertagia	
21	27	56.2	91	1	R37A_CHICK	P32046 gallus gall	
22	27	56.2	91	1	R37A_HUMAN	P12751 homo sapien	
23	27	56.2	91	1	R37A_ICTPU	Q90yt0 ictalurus p	
24	26	54.2	52	1	RC21_ARATH	Q9fe70 arabidopsis	
25	26	54.2	57	1	GRN1_CYPCA	P81013 cyprinus ca	
26	26	54.2	57	1	GRN2_CYPCA	P81014 cyprinus ca	
27	26	54.2	57	1	GRN3_CYPCA	P81015 cyprinus ca	
28	26	54.2	61	1	RUB2_DESDE	Q93pp8 desulfovibr	

29	26	54.2	69	1	TOX1_OXYKI	P83288	oxyopes kit
30	26	54.2	70	1	R37A_SULSO	Q97zq3	sulfolobus
31	26	54.2	70	1	R37A_SULTO	Q975h0	sulfolobus
32	26	54.2	72	1	YF77_HAEIN	Q57070	haemophilus
33	26	54.2	83	1	YVAO_VACCC	P20524	vaccinia vi
34	26	54.2	89	1	BARS_BACAM	P11540	bacillus am
35	26	54.2	91	1	RL43_YEAST	P49631	saccharomyc
36	25	52.1	23	1	CR41_LITCE	P56242	litoria cae
37	25	52.1	23	1	CR42_LITCE	P56243	litoria cae
38	25	52.1	29	1	CXD6_CONGL	Q9twm7	conus glori
39	25	52.1	31	1	PETN_CYACA	Q9tlr6	cyanidium c
40	25	52.1	45	1	Y5K6_SSV1	P20198	sulfolobus
41	25	52.1	52	1	RUBR_CLOTS	P19500	clostridium
42	25	52.1	54	1	LT01_HORVU	Q42509	hordeum vul
43	25	52.1	54	1	LT02_HORVU	Q9ard5	hordeum vul
44	25	52.1	77	1	TXL1_PHONI	P17727	phoneutria
45	25	52.1	80	1	R37A_THEVO	Q97bz3	thermoplasm

Title: US-09-929-924-13
Perfect score: 48
Sequence: 1 GMWQCLLS 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 175362

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_25:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		%					
No.	Score	Match	Length	DB	ID	Description	
1	45	93.8	90	11	P70443	P70443 mus musculu	
2	37	77.1	71	6	Q8HY42	Q8hy42 bos taurus	
3	37	77.1	71	6	Q8HY28	Q8hy28 ovis aries	
4	34	70.8	75	5	Q9NC72	Q9nc72 oxytricha t	
5	34	70.8	77	10	Q8RW18	Q8rwl8 prunus pers	
6	34	70.8	78	6	Q28373	Q28373 equus cabal	
7	32	66.7	49	12	Q00695	Q00695 hepatitis c	
8	32	66.7	74	12	Q81567	Q81567 hepatitis c	
9	32	66.7	75	2	P94839	P94839 helicobacte	
10	32	66.7	80	12	Q81572	Q81572 hepatitis c	
11	32	66.7	80	12	Q81593	Q81593 hepatitis c	

12	32	66.7	80	12	Q81562	Q81562 hepatitis c
13	32	66.7	80	12	Q81750	Q81750 hepatitis c
14	32	66.7	88	16	Q81FK4	Q81fk4 bacillus ce
15	32	66.7	92	16	Q8XTF4	Q8xtf4 ralstonia s
16	31	64.6	28	5	Q86GJ7	Q86gj7 leptinotars
17	31	64.6	28	5	Q86GJ5	Q86gj5 leptinotars
18	31	64.6	31	2	O52911	O52911 campylobact
19	31	64.6	49	12	Q00694	Q00694 hepatitis c
20	31	64.6	58	5	Q7Z0Z1	Q7z0z1 ochlerotatu
21	31	64.6	58	5	Q7Z0Z0	Q7z0z0 ochlerotatu
22	31	64.6	58	5	Q7Z0Y9	Q7z0y9 aedes trise
23	31	64.6	58	5	Q7Z0Y8	Q7z0y8 aedes trise
24	31	64.6	58	5	Q7Z0Y7	Q7z0y7 ochlerotatu
25	31	64.6	58	5	Q7Z0Y6	Q7z0y6 ochlerotatu
26	31	64.6	58	5	Q7Z0Y5	Q7z0y5 ochlerotatu
27	31	64.6	58	5	Q7Z0Y4	Q7z0y4 culex pipie
28	31	64.6	58	5	Q7Z0Y3	Q7z0y3 culex terri
29	31	64.6	58	5	Q7Z0Y2	Q7z0y2 culex restu
30	31	64.6	58	5	Q7Z0Y1	Q7z0y1 aedes vexan
31	31	64.6	58	5	Q7Z0Y0	Q7z0y0 aedes ciner
32	31	64.6	58	5	Q7YSS0	Q7yss0 aedes vexan
33	31	64.6	58	5	Q7YSR9	Q7ysr9 anopheles p
34	31	64.6	58	5	Q7YSR8	Q7ysr8 ochlerotatu
35	31	64.6	79	2	Q02306	Q02306 pseudomonas
36	31	64.6	82	16	P72992	P72992 synechocyst
37	31	64.6	98	12	O41079	O41079 paramecium
38	31	64.6	100	16	P74472	P74472 synechocyst
39	31	64.6	100	16	Q55567	Q55567 synechocyst
40	30	62.5	44	2	Q933Q1	Q933q1 ureaplasma
41	30	62.5	52	10	Q9SWZ1	Q9swz1 lycopersico
42	30	62.5	60	16	Q9PEL4	Q9pel4 xylella fas
43	30	62.5	63	16	Q8G0C8	Q8g0c8 brucella su
44	30	62.5	68	10	Q8W0L3	Q8w0l3 oryza sativ
45	30	62.5	69	13	Q9I894	Q9i894 oncorhynch

Title: US-09-929-924-14
 Perfect score: 69
 Sequence: 1 TGLWQCLLSEGD 12

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 891005

Minimum DB seq length: 0
 Maximum DB seq length: 100

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
 1: geneseqp1980s:*
 2: geneseqp1990s:*
 3: geneseqp2000s:*
 4: geneseqp2001s:*
 5: geneseqp2002s:*
 6: geneseqp2003as:*
 7: geneseqp2003bs:*
 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		%					Description
Result	Query	Match	Length	DB	ID		
No.	Score						
1	69	100.0	12	4	AAB70016	Aab70016 Mammalian	
2	69	100.0	72	4	AAB70019	Aab70019 Mammalian	
3	47	68.1	16	4	AAB70014	Aab70014 Mammalian	
4	47	68.1	21	4	AAB89248	Aab89248 HIV gp120	
5	47	68.1	21	4	AAB89247	Aab89247 HIV gp120	
6	47	68.1	21	4	AAB89249	Aab89249 HIV gp120	
7	47	68.1	73	4	AAB70018	Aab70018 Mammalian	
8	45	65.2	8	4	AAB70015	Aab70015 Mammalian	
9	45	65.2	73	4	AAB70029	Aab70029 Human CD4	
10	45	65.2	73	4	AAB70028	Aab70028 Human CD4	
11	43	62.3	95	4	AAU21547	Aau21547 Human nov	
12	42	60.9	73	4	AAB70025	Aab70025 Human CD4	
13	41	59.4	65	5	ABP08385	Abp08385 Human ORF	
14	41	59.4	73	4	AAB70026	Aab70026 Human CD4	
15	41	59.4	73	4	AAB70027	Aab70027 Human CD4	
16	39	56.5	24	2	AAY12811	Aay12811 Human 5'	
17	38	55.1	73	4	AAU56149	Aau56149 Propionib	
18	38	55.1	73	6	ABM52668	Abm52668 Propionib	
19	38	55.1	99	2	AAR33742	Aar33742 hXR1prime	
20	37	53.6	6	4	AAB70006	Aab70006 Mammalian	

21	37	53.6	16	6	ABP82724	Abp82724	G protein
22	37	53.6	20	4	ABB44940	Abb44940	Rabbit al
23	37	53.6	21	4	AAB89246	Aab89246	HIV gp120
24	37	53.6	51	4	AAU56911	Aau56911	Propionib
25	37	53.6	51	6	ABM53430	Abm53430	Propionib
26	37	53.6	61	2	AAY12082	Aay12082	Human 5'
27	37	53.6	63	4	AAM94617	Aam94617	Human rep
28	37	53.6	100	4	ABG16553	Abg16553	Novel hum
29	36	52.2	20	4	ABB45153	Abb45153	Rat album
30	36	52.2	21	2	AAW13415	Aaw13415	Brain hom
31	36	52.2	21	3	AAB12002	Aab12002	Brain hom
32	36	52.2	21	4	AAE11808	Aae11808	Phage pep
33	36	52.2	21	5	AAU10719	Aau10719	Brain hom
34	36	52.2	21	6	ABU59531	Abu59531	Brain rec
35	36	52.2	21	7	ADC33703	Adc33703	Brain cel
36	36	52.2	31	4	AAM37243	Aam37243	Peptide #
37	36	52.2	67	4	AAU45497	Aau45497	Propionib
38	36	52.2	67	6	ABM42016	Abm42016	Propionib
39	36	52.2	86	5	ABP02409	Abp02409	Human ORF
40	35.5	51.4	58	7	ADC22991	Adc22991	Conserved
41	35.5	51.4	58	7	ADC23167	Adc23167	Conserved
42	35.5	51.4	85	4	AAM86004	Aam86004	Human imm
43	35	50.7	18	4	ABB45252	Abb45252	Rabbit al
44	35	50.7	49	6	ABU07226	Abu07226	Maize SSI
45	35	50.7	49	6	ABU07227	Abu07227	Maize SSI

Title: US-09-929-924-14
Perfect score: 69
Sequence: 1 TGLWQCLLSEGD 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 264921

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	47	68.1	83	2	US-08-332-562A-87	Sequence 87, Appl
2	38	55.1	99	1	US-08-333-358-4	Sequence 4, Appli
3	38	55.1	99	1	US-08-463-694-4	Sequence 4, Appli
4	38	55.1	99	1	US-08-694-501-4	Sequence 4, Appli
5	36	52.2	21	1	US-08-526-710-16	Sequence 16, Appl
6	36	52.2	21	3	US-08-862-855-16	Sequence 16, Appl
7	36	52.2	21	3	US-09-226-985-16	Sequence 16, Appl
8	36	52.2	21	4	US-09-227-906-16	Sequence 16, Appl
9	35	50.7	68	4	US-09-312-283C-376	Sequence 376, App
10	35	50.7	87	2	US-08-477-451-45	Sequence 45, Appl
11	35	50.7	91	4	US-09-543-681A-8118	Sequence 8118, Ap
12	34	49.3	30	4	US-08-857-636-67	Sequence 67, Appl
13	34	49.3	99	1	US-08-036-210-27	Sequence 27, Appl
14	34	49.3	99	2	US-08-449-609-27	Sequence 27, Appl
15	34	49.3	99	4	US-09-361-096A-27	Sequence 27, Appl
16	33	47.8	16	4	US-08-469-260A-345	Sequence 345, App
17	33	47.8	16	4	US-08-488-446-345	Sequence 345, App
18	33	47.8	16	4	US-08-467-344A-345	Sequence 345, App
19	33	47.8	36	4	US-09-069-827A-49	Sequence 49, Appl
20	33	47.8	44	4	US-09-369-247-94	Sequence 94, Appl
21	32.5	47.1	21	1	US-08-484-635-96	Sequence 96, Appl
22	32.5	47.1	21	2	US-08-484-631-96	Sequence 96, Appl

23	32.5	47.1	21	2	US-08-827-570-96	Sequence 96, Appl
24	32	46.4	73	4	US-08-469-260A-36	Sequence 36, Appl
25	32	46.4	73	4	US-08-488-446-36	Sequence 36, Appl
26	32	46.4	73	4	US-08-467-344A-36	Sequence 36, Appl
27	32	46.4	87	4	US-09-621-976-4119	Sequence 4119, Ap
28	32	46.4	100	4	US-09-025-596-80	Sequence 80, Appl
29	32	46.4	100	4	US-09-073-661-80	Sequence 80, Appl
30	32	46.4	100	4	US-10-100-785-80	Sequence 80, Appl
31	31	44.9	28	4	US-09-187-789-50	Sequence 50, Appl
32	31	44.9	28	4	US-09-139-600-45	Sequence 45, Appl
33	31	44.9	42	4	US-09-904-615-82	Sequence 82, Appl
34	31	44.9	52	4	US-10-138-158-21	Sequence 21, Appl
35	31	44.9	68	4	US-09-673-395A-383	Sequence 383, App
36	31	44.9	79	4	US-09-621-976-6689	Sequence 6689, Ap
37	31	44.9	100	6	5252466-19	Patent No. 5252466
38	30	43.5	12	2	US-08-556-597-137	Sequence 137, App
39	30	43.5	26	3	US-09-224-785-38	Sequence 38, Appl
40	30	43.5	26	4	US-09-756-594-38	Sequence 38, Appl
41	30	43.5	32	4	US-09-698-286A-35	Sequence 35, Appl
42	30	43.5	41	2	US-08-838-957A-19	Sequence 19, Appl
43	30	43.5	54	4	US-09-205-258-280	Sequence 280, App
44	30	43.5	81	2	US-08-332-562A-86	Sequence 86, Appl
45	30	43.5	87	4	US-09-489-039A-14038	Sequence 14038, A

Title: US-09-929-924-14
 Perfect score: 69
 Sequence: 1 TGLWQCLLSEGD 12

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 1276540 seqs, 311283816 residues

Total number of hits satisfying chosen parameters: 533274

Minimum DB seq length: 0
 Maximum DB seq length: 100

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Published_Applications_AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
- 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	%		DB	ID	Description
		Query	Match Length			
1	69	100.0	12	9	US-09-929-924-14	Sequence 14, Appl
2	69	100.0	72	9	US-09-929-924-17	Sequence 17, Appl
3	47	68.1	16	9	US-09-929-924-12	Sequence 12, Appl
4	47	68.1	21	14	US-10-084-813-354	Sequence 354, App
5	47	68.1	21	14	US-10-084-813-355	Sequence 355, App
6	47	68.1	21	14	US-10-084-813-356	Sequence 356, App
7	47	68.1	73	9	US-09-929-924-16	Sequence 16, Appl
8	45	65.2	8	9	US-09-929-924-13	Sequence 13, Appl
9	45	65.2	73	9	US-09-929-924-36	Sequence 36, Appl
10	45	65.2	73	9	US-09-929-924-37	Sequence 37, Appl

11	45	65.2	83	9	US-09-771-161A-108	Sequence 108, App
12	42	60.9	51	14	US-10-029-386-29257	Sequence 29257, A
13	42	60.9	73	9	US-09-929-924-33	Sequence 33, Appl
14	41	59.4	73	9	US-09-929-924-34	Sequence 34, Appl
15	41	59.4	73	9	US-09-929-924-35	Sequence 35, Appl
16	40	58.0	85	16	US-10-437-963-188986	Sequence 188986,
17	39	56.5	94	12	US-10-424-599-279667	Sequence 279667,
18	38	55.1	87	12	US-10-424-599-227804	Sequence 227804,
19	37	53.6	6	9	US-09-929-924-4	Sequence 4, Appli
20	37	53.6	16	14	US-10-225-567A-1397	Sequence 1397, Ap
21	37	53.6	20	15	US-10-186-229-28	Sequence 28, Appl
22	37	53.6	21	14	US-10-084-813-353	Sequence 353, App
23	37	53.6	63	10	US-09-764-891-3275	Sequence 3275, Ap
24	37	53.6	69	16	US-10-437-963-124432	Sequence 124432,
25	37	53.6	72	12	US-10-425-114-39707	Sequence 39707, A
26	37	53.6	87	12	US-10-424-599-195884	Sequence 195884,
27	37	53.6	87	12	US-10-425-114-54309	Sequence 54309, A
28	36	52.2	20	15	US-10-186-229-205	Sequence 205, App
29	36	52.2	21	12	US-09-912-609-5	Sequence 5, Appli
30	36	52.2	21	12	US-09-922-227-16	Sequence 16, Appl
31	36	52.2	31	9	US-09-864-761-48807	Sequence 48807, A
32	36	52.2	49	14	US-10-029-386-31033	Sequence 31033, A
33	36	52.2	51	14	US-10-029-386-31895	Sequence 31895, A
34	36	52.2	58	12	US-10-424-599-195214	Sequence 195214,
35	36	52.2	64	12	US-10-424-599-212323	Sequence 212323,
36	36	52.2	66	12	US-10-424-599-249944	Sequence 249944,
37	36	52.2	70	16	US-10-437-963-156831	Sequence 156831,
38	36	52.2	80	14	US-10-029-386-29168	Sequence 29168, A
39	35	50.7	18	15	US-10-186-229-326	Sequence 326, App
40	35	50.7	49	16	US-10-109-048-1132	Sequence 1132, Ap
41	35	50.7	49	16	US-10-109-048-1133	Sequence 1133, Ap
42	35	50.7	50	10	US-09-764-891-4874	Sequence 4874, Ap
43	35	50.7	50	12	US-10-424-599-176845	Sequence 176845,
44	35	50.7	50	14	US-10-205-428-399	Sequence 399, App
45	35	50.7	51	16	US-10-109-048-640	Sequence 640, App

Title: US-09-929-924-14
 Perfect score: 69
 Sequence: 1 TGLWQCLLSEGD 12

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 37674

Minimum DB seq length: 0
 Maximum DB seq length: 100

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : PIR_78:*
 1: pir1:*
 2: pir2:*
 3: pir3:*
 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		%	Query				
No.	Score	Match	Length	DB	ID	Description	
1	38	55.1	83	2	E75218	ribosomal protein	
2	38	55.1	86	2	B71204	ribosomal protein	
3	35	50.7	83	2	A69257	ribosomal protein	
4	34	49.3	70	2	E83791	hypothetical prote	
5	33	47.8	79	2	S24379	hypothetical prote	
6	33	47.8	82	2	S74971	transposase ssr269	
7	33	47.8	91	2	T26996	ribosomal protein	
8	33	47.8	100	2	S76444	transposase slr016	
9	33	47.8	100	2	S76090	transposase sll016	
10	32	46.4	63	2	AC2278	hypothetical prote	
11	32	46.4	82	2	D84387	hypothetical prote	
12	32	46.4	82	2	A98165	insertion element	
13	32	46.4	82	2	G98128	insertion element	
14	32	46.4	91	1	MNVUAV	nonstructural prot	
15	32	46.4	91	2	A97004	barstar-like prote	
16	31.5	45.7	90	2	AD2020	hypothetical prote	
17	31	44.9	39	2	I46149	aldolase A - dog (
18	31	44.9	39	2	I57685	aldolase A - south	
19	31	44.9	60	2	B82733	hypothetical prote	
20	31	44.9	62	2	S25999	hypothetical prote	
21	31	44.9	80	2	AD1134	hypothetical prote	
22	31	44.9	87	2	T18182	hypothetical prote	
23	31	44.9	89	2	H86867	prophage ps3 prote	
24	31	44.9	98	2	T18099	hypothetical prote	

25	30.5	44.2	56	2	S45028	sox2 protein - Her
26	30.5	44.2	62	2	A82857	hypothetical prote
27	30	43.5	30	2	A03148	retinol-binding pr
28	30	43.5	75	2	G01571	growth hormone-rel
29	30	43.5	92	1	S36658	proteinase inhibit
30	30	43.5	94	2	AG2364	hypothetical prote
31	29	42.0	30	2	I52254	gene CYP11B2 prote
32	29	42.0	36	2	A81740	hypothetical prote
33	29	42.0	37	2	C60580	growth hormone-rel
34	29	42.0	40	2	T07472	hypothetical prote
35	29	42.0	50	2	F71281	hypothetical prote
36	29	42.0	62	2	S22564	finger protein - h
37	29	42.0	67	2	H75308	hypothetical prote
38	29	42.0	70	2	G84110	hypothetical prote
39	29	42.0	72	2	E44915	rubredoxin homolog
40	29	42.0	72	2	S53661	hydrogenase-relate
41	29	42.0	73	2	AE3264	hypothetical prote
42	29	42.0	77	2	AE2043	hypothetical prote
43	29	42.0	78	1	W5WL41	E5 protein - human
44	29	42.0	81	2	AG0142	molybdopterin [mpt
45	29	42.0	87	2	C85825	hypothetical prote

Title: US-09-929-924-14
 Perfect score: 69
 Sequence: 1 TGLWQCLLSEGD 12

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 15046

Minimum DB seq length: 0
 Maximum DB seq length: 100

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		%					
Result		Query					
No.	Score	Match	Length	DB	ID	Description	
1	38	55.1	83	1	R37A_PYRAB	Q9v202	pyrococcus
2	38	55.1	83	1	R37A_PYRFU	Q8tzi4	pyrococcus
3	38	55.1	83	1	R37A_PYRHO	O74106	pyrococcus
4	38	55.1	95	1	R37A_HALN1	Q9hsg8	halobacteri
5	35	50.7	83	1	R37A_ARCFU	O30179	archaeoglob
6	34	49.3	89	1	R37A_METKA	Q8tyc3	methanopyru
7	33	47.8	80	1	R37A_THEAC	Q9hip0	thermoplasm
8	33	47.8	89	1	CFA_CITFR	P45509	citrobacter
9	32	46.4	91	1	VNST_AINOV	P12413	aino virus.
10	31	44.9	62	1	YM32_MARPO	P38474	marchantia
11	30	43.5	91	1	R37A_SCHMA	O17307	schistosoma
12	30	43.5	92	1	LCM_LOCFI	P80060	locusta mig
13	29	42.0	37	1	GHR3_RAT	P33580	rattus norv
14	29	42.0	50	1	Y799_TREPA	O83777	treponema p
15	29	42.0	72	1	RUBR_AZOCH	P48343	azotobacter
16	29	42.0	72	1	RUBR_AZOVI	P30778	azotobacter
17	29	42.0	78	1	VE5_HP41	P27554	human papil
18	29	42.0	82	1	FGF8_CANFA	O62682	canis famil
19	29	42.0	89	1	R37A_METTH	O26777	methanobact
20	29	42.0	94	1	RL43_SCHPO	O94686	schizosacch
21	29	42.0	95	1	YHEL_ECOLI	P45530	escherichia
22	29	42.0	95	1	YPSS_RHILP	P10497	rhizobium l
23	29	42.0	96	1	R37A_PLAFA	O96184	plasmodium
24	28	40.6	33	1	CXBW_CONRA	P58804	conus radia
25	28	40.6	39	1	TX4K_EURCA	P18928	eurypelma c
26	28	40.6	70	1	R37A_SULSO	Q97zq3	sulfolobus
27	28	40.6	85	1	R37A_MYXGL	Q9y0h7	myxine glut
28	28	40.6	89	1	BARS_BACAM	P11540	bacillus am

29	28	40.6	90	1	R37A_OSTOS	O61598	ostertagia
30	28	40.6	91	1	R37A_CHICK	P32046	gallus gall
31	28	40.6	91	1	R37A_HUMAN	P12751	homo sapien
32	28	40.6	91	1	R37A ICTPU	Q90yt0	ictalurus p
33	27.5	39.9	23	1	CR41_LITCE	P56242	litoria cae
34	27.5	39.9	23	1	CR42_LITCE	P56243	litoria cae
35	27	39.1	17	1	CXMA_CONPE	P58926	conus penna
36	27	39.1	67	1	RPBX_DROME	Q9vc49	drosophila
37	27	39.1	67	1	RPBX_HUMAN	P52436	homo sapien
38	27	39.1	70	1	R37A_SULTO	Q975h0	sulfolobus
39	27	39.1	71	1	ARRD_RAT	P36577	rattus norv
40	27	39.1	72	1	YBDZ_ECOLI	P18393	escherichia
41	27	39.1	72	1	YF77_HAEIN	Q57070	haemophilus
42	27	39.1	77	1	IF1C_AMBTC	Q95gn9	amborella t
43	27	39.1	83	1	YVAO_VACCC	P20524	vaccinia vi
44	27	39.1	86	1	R37A_AERPE	Q9yc06	aeropyrum p
45	27	39.1	88	1	RS16_MYCPN	P75131	mycoplasma

Title: US-09-929-924-14
 Perfect score: 69
 Sequence: 1 TGLWQCLLSEGD 12

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 175362

Minimum DB seq length: 0
 Maximum DB seq length: 100

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : SPTREMBL_25:*
 1: sp_archaea:*
 2: sp_bacteria:*
 3: sp_fungi:*
 4: sp_human:*
 5: sp_invertebrate:*
 6: sp_mammal:*
 7: sp_mhc:*
 8: sp_organelle:*
 9: sp_phage:*
 10: sp_plant:*
 11: sp_rodent:*
 12: sp_virus:*
 13: sp_vertibrate:*
 14: sp_unclassified:*
 15: sp_rvirus:*
 16: sp_bacteriap:*
 17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	69	100.0	90	11	P70443	P70443 mus musculu
2	40	58.0	85	10	Q7XWU7	Q7xwu7 oryza sativ
3	39	56.5	71	6	Q8HY42	Q8hy42 bos taurus
4	39	56.5	71	6	Q8HY28	Q8hy28 ovis aries
5	36	52.2	56	16	Q8FZ17	Q8fz17 brucella su
6	36	52.2	77	10	Q8RW18	Q8rw18 prunus pers
7	35	50.7	69	13	Q9I894	Q9i894 oncorhynch
8	35	50.7	75	2	P94839	P94839 helicobacte
9	35	50.7	75	5	Q9NC72	Q9nc72 oxytricha t
10	35	50.7	75	10	Q8L513	Q8l513 oryza sativ
11	34	49.3	70	16	Q9KDS8	Q9kds8 bacillus ha

12	34	49.3	78	6	Q28373	Q28373 equus cabal
13	34	49.3	83	2	Q8VVD4	Q8vvd4 salmonella
14	34	49.3	92	16	Q9RD62	Q9rd62 streptomyce
15	34	49.3	94	17	Q8TPX8	Q8tpx8 methanosarc
16	34	49.3	94	17	Q8PTT6	Q8ptt6 methanosarc
17	33.5	48.6	58	16	Q8NU83	Q8nu83 corynebacte
18	33	47.8	55	5	Q27187	Q27187 paramecium
19	33	47.8	55	9	Q854Y1	Q854y1 mycobacteri
20	33	47.8	61	10	Q7XIP3	Q7xip3 oryza sativ
21	33	47.8	66	17	Q8ZZX5	Q8zzx5 pyrobaculum
22	33	47.8	67	16	Q8FJV2	Q8fjv2 escherichia
23	33	47.8	79	2	Q02306	Q02306 pseudomonas
24	33	47.8	82	16	P72992	P72992 synechocyst
25	33	47.8	91	5	Q9U2A8	Q9u2a8 caenorhabdi
26	33	47.8	100	16	P74472	P74472 synechocyst
27	33	47.8	100	16	Q55567	Q55567 synechocyst
28	32	46.4	31	2	O52911	O52911 campylobact
29	32	46.4	34	16	Q8KEC8	Q8kec8 chlorobium
30	32	46.4	63	16	Q8YQP2	Q8yqp2 anabaena sp
31	32	46.4	77	3	Q96WC0	Q96wc0 hirsutella
32	32	46.4	77	3	Q96WC5	Q96wc5 hirsutella
33	32	46.4	77	3	Q96WE1	Q96we1 hirsutella
34	32	46.4	82	17	Q9H MV7	Q9hmv7 halobacteri
35	32	46.4	88	16	Q81FK4	Q81fk4 bacillus ce
36	32	46.4	91	12	Q8QZ60	Q8qz60 douglas vir
37	32	46.4	91	12	Q8QZ37	Q8qz37 shuni virus
38	32	46.4	91	12	Q8QZ58	Q8qz58 kaikalur vi
39	32	46.4	91	12	Q8QPV6	Q8qpv6 peaton viru
40	32	46.4	91	12	Q8QZ39	Q8qz39 shamonda vi
41	32	46.4	91	12	Q8QHN1	Q8qhn1 peaton viru
42	32	46.4	91	16	Q97KS3	Q97ks3 clostridium
43	31.5	45.7	50	17	Q9HI15	Q9hi15 halobacteri
44	31.5	45.7	63	16	Q7UYL3	Q7uyl3 rhodopirell
45	31.5	45.7	90	16	Q8YWA1	Q8ywa1 anabaena sp

Title: US-09-929-924-15
 Perfect score: 53
 Sequence: 1 VSEEQKVVQVVA 12

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 891005

Minimum DB seq length: 0
 Maximum DB seq length: 100

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
 1: geneseqp1980s:*
 2: geneseqp1990s:*
 3: geneseqp2000s:*
 4: geneseqp2001s:*
 5: geneseqp2002s:*
 6: geneseqp2003as:*
 7: geneseqp2003bs:*
 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	53	100.0	12	4	AAB70017	Aab70017 Mammalian
2	53	100.0	72	4	AAB70019	Aab70019 Mammalian
3	35	66.0	51	2	AAW83320	Aaw83320 SIP1 mini
4	32	60.4	93	7	ADC94062	Adc94062 E. faeciu
5	31	58.5	50	4	AAB62001	Aab62001 A-myb pro
6	31	58.5	50	4	AAB62000	Aab62000 B-myb pro
7	31	58.5	50	4	AAB62002	Aab62002 C-myb pro
8	30	56.6	13	2	AAR72559	Aar72559 Rat manno
9	30	56.6	13	2	AAY41830	Aay41830 Rat manno
10	30	56.6	13	2	AAW95240	Aaw95240 Rat manno
11	30	56.6	13	3	AAY68379	Aay68379 Mannose b
12	30	56.6	13	4	AAB66253	Aab66253 MBP C-ter
13	30	56.6	35	4	AAE10942	Aae10942 Mouse mas
14	30	56.6	51	5	AAE16016	Aae16016 Human ga_
15	30	56.6	63	7	ABR63039	Abr63039 Z-alpha d
16	30	56.6	67	4	AAM65659	Aam65659 Human bra
17	30	56.6	70	2	AAW77395	Aaw77395 Streptoco
18	30	56.6	70	2	AAW71313	Aaw71313 Streptoco
19	30	56.6	76	4	ABG23009	Abg23009 Novel hum
20	30	56.6	95	5	ABP31519	Abp31519 Human ORF

21	29	54.7	13	3	AAAY80135	Aay80135	Lipocorti
22	29	54.7	13	7	ADB67685	Adb67685	Glucocort
23	29	54.7	14	4	AAU68234	Aau68234	Human Bre
24	29	54.7	25	3	AAAY80134	Aay80134	Lipocorti
25	29	54.7	25	7	ADB67684	Adb67684	Glucocort
26	29	54.7	29	6	ABR62731	Abr62731	Human ann
27	29	54.7	59	4	AAM18925	Aam18925	Peptide #
28	29	54.7	59	4	ABB38070	Abb38070	Peptide #
29	29	54.7	59	4	AAM31493	Aam31493	Peptide #
30	29	54.7	59	4	ABB23291	Abb23291	Protein #
31	29	54.7	59	4	AAM71212	Aam71212	Human bon
32	29	54.7	59	4	AAM58706	Aam58706	Human bra
33	29	54.7	59	4	ABG52924	Abg52924	Human liv
34	29	54.7	59	5	ABG41009	Abg41009	Human pep
35	29	54.7	64	4	AAM88786	Aam88786	Human imm
36	29	54.7	70	4	AAM18441	Aam18441	Peptide #
37	29	54.7	70	4	ABB37480	Abb37480	Peptide #
38	29	54.7	70	4	ABB32232	Abb32232	Peptide #
39	29	54.7	70	4	AAM58150	Aam58150	Human bra
40	29	54.7	70	5	ABG40278	Abg40278	Human pep
41	29	54.7	77	5	ABP64081	Abp64081	Human ORF
42	29	54.7	80	2	AAW71717	Aaw71717	Clavanin
43	29	54.7	80	2	AAW63626	Aaw63626	Antimicro
44	29	54.7	80	5	AAE22172	Aae22172	Human 184
45	29	54.7	88	7	ADC89173	Adc89173	Ribosomal

Title: US-09-929-924-15
Perfect score: 53
Sequence: 1 VSEEQKVVQVVA 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 264921

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		%					
No.	Score	Match	Length	DB	ID	Description	
1	35	66.0	51	4	US-09-449-285A-21	Sequence 21, Appl	
2	32	60.4	93	4	US-09-107-532A-3689	Sequence 3689, Ap	
3	31	58.5	50	3	US-09-156-316-4	Sequence 4, Appli	
4	31	58.5	50	3	US-09-156-316-5	Sequence 5, Appli	
5	31	58.5	50	3	US-09-156-316-6	Sequence 6, Appli	
6	30	56.6	13	2	US-08-292-968-40	Sequence 40, Appl	
7	30	56.6	13	2	US-08-467-974-40	Sequence 40, Appl	
8	30	56.6	13	2	US-08-467-536-40	Sequence 40, Appl	
9	30	56.6	13	3	US-08-467-976-40	Sequence 40, Appl	
10	30	56.6	13	3	US-09-082-514-40	Sequence 40, Appl	
11	29	54.7	20	3	US-08-505-250-16	Sequence 16, Appl	
12	29	54.7	20	4	US-08-505-250-16	Sequence 16, Appl	
13	29	54.7	80	2	US-08-808-277A-3	Sequence 3, Appli	
14	29	54.7	80	3	US-08-746-160-3	Sequence 3, Appli	
15	29	54.7	88	4	US-09-732-210-1426	Sequence 1426, Ap	
16	28	52.8	9	1	US-08-178-570-64	Sequence 64, Appl	
17	28	52.8	9	3	US-08-369-643-64	Sequence 64, Appl	
18	28	52.8	9	5	PCT-US95-00147-64	Sequence 64, Appl	
19	28	52.8	34	4	US-09-202-161B-30	Sequence 30, Appl	
20	28	52.8	52	1	US-08-519-103-13	Sequence 13, Appl	
21	28	52.8	52	3	US-09-018-635-13	Sequence 13, Appl	
22	28	52.8	52	4	US-09-912-962-13	Sequence 13, Appl	

23	28	52.8	57	4	US-09-696-169A-21	Sequence 21, Appl
24	28	52.8	59	4	US-09-288-143-79	Sequence 79, Appl
25	28	52.8	76	4	US-09-504-132-22	Sequence 22, Appl
26	28	52.8	84	4	US-09-540-236-2734	Sequence 2734, Ap
27	27	50.9	9	2	US-08-621-803-195	Sequence 195, App
28	27	50.9	9	3	US-09-217-352-195	Sequence 195, App
29	27	50.9	46	4	US-09-530-139-12	Sequence 12, Appl
30	27	50.9	52	1	US-08-519-103-14	Sequence 14, Appl
31	27	50.9	52	3	US-09-018-635-14	Sequence 14, Appl
32	27	50.9	52	4	US-09-912-962-14	Sequence 14, Appl
33	27	50.9	53	4	US-09-621-976-6827	Sequence 6827, Ap
34	27	50.9	66	2	US-08-162-081B-42	Sequence 42, Appl
35	27	50.9	66	2	US-08-780-872-42	Sequence 42, Appl
36	27	50.9	66	3	US-09-085-957-42	Sequence 42, Appl
37	27	50.9	80	4	US-09-543-681A-8028	Sequence 8028, Ap
38	27	50.9	83	1	US-08-260-202A-17	Sequence 17, Appl
39	27	50.9	94	4	US-09-621-976-6341	Sequence 6341, Ap
40	27	50.9	95	4	US-08-858-207A-516	Sequence 516, App
41	27	50.9	98	3	US-09-062-440-10	Sequence 10, Appl
42	27	50.9	98	4	US-09-712-495-10	Sequence 10, Appl
43	27	50.9	99	4	US-09-328-352-4669	Sequence 4669, Ap
44	26	49.1	20	1	US-07-940-861-4	Sequence 4, Appli
45	26	49.1	20	1	US-08-459-512-4	Sequence 4, Appli

Title: US-09-929-924-15
Perfect score: 53
Sequence: 1 VSEEQKVVQVVA 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1276540 seqs, 311283816 residues

Total number of hits satisfying chosen parameters: 533274

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
- 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	%		DB	ID	Description
		Query	Match Length			
1	53	100.0	12	9	US-09-929-924-15	Sequence 15, Appl
2	53	100.0	72	9	US-09-929-924-17	Sequence 17, Appl
3	36	67.9	67	14	US-10-083-357-851	Sequence 851, App
4	35	66.0	51	9	US-09-964-238-21	Sequence 21, Appl
5	33	62.3	89	12	US-10-424-599-266038	Sequence 266038,
6	32	60.4	57	14	US-10-293-086-123	Sequence 123, App
7	32	60.4	65	16	US-10-437-963-203925	Sequence 203925,
8	32	60.4	73	14	US-10-029-386-29085	Sequence 29085, A
9	31	58.5	50	9	US-09-757-049A-4	Sequence 4, Appli
10	31	58.5	50	9	US-09-757-049A-5	Sequence 5, Appli

11	31	58.5	50	9	US-09-757-049A-6	Sequence 6, Appli
12	31	58.5	82	12	US-10-424-599-280433	Sequence 280433,
13	31	58.5	86	12	US-10-424-599-211464	Sequence 211464,
14	31	58.5	90	12	US-10-424-599-231423	Sequence 231423,
15	30	56.6	35	12	US-10-423-483-21	Sequence 21, Appl
16	30	56.6	35	15	US-10-220-587-21	Sequence 21, Appl
17	30	56.6	51	10	US-09-851-873-47	Sequence 47, Appl
18	30	56.6	56	12	US-10-424-599-270420	Sequence 270420,
19	30	56.6	63	12	US-10-321-785-7	Sequence 7, Appli
20	30	56.6	67	9	US-09-864-761-46429	Sequence 46429, A
21	30	56.6	71	12	US-10-424-599-169243	Sequence 169243,
22	30	56.6	73	12	US-10-424-599-229964	Sequence 229964,
23	30	56.6	95	11	US-09-864-408A-984	Sequence 984, App
24	30	56.6	100	16	US-10-437-963-146206	Sequence 146206,
25	29	54.7	13	10	US-09-759-484-7	Sequence 7, Appli
26	29	54.7	14	12	US-09-988-493-158	Sequence 158, App
27	29	54.7	25	10	US-09-759-484-6	Sequence 6, Appli
28	29	54.7	49	12	US-10-424-599-246346	Sequence 246346,
29	29	54.7	52	14	US-10-097-534-54	Sequence 54, Appl
30	29	54.7	59	9	US-09-864-761-38589	Sequence 38589, A
31	29	54.7	70	9	US-09-864-761-43146	Sequence 43146, A
32	29	54.7	71	12	US-10-424-599-267093	Sequence 267093,
33	29	54.7	77	9	US-09-867-550-902	Sequence 902, App
34	29	54.7	77	12	US-10-424-599-238882	Sequence 238882,
35	29	54.7	80	9	US-09-910-150-22	Sequence 22, Appl
36	29	54.7	80	12	US-10-377-097-22	Sequence 22, Appl
37	29	54.7	89	13	US-10-013-379-38	Sequence 38, Appl
38	29	54.7	89	14	US-10-340-578-22	Sequence 22, Appl
39	29	54.7	95	9	US-09-910-150-18	Sequence 18, Appl
40	29	54.7	95	9	US-09-910-150-20	Sequence 20, Appl
41	29	54.7	95	12	US-10-377-097-18	Sequence 18, Appl
42	29	54.7	95	12	US-10-377-097-20	Sequence 20, Appl
43	29	54.7	95	16	US-10-437-963-121279	Sequence 121279,
44	28	52.8	6	9	US-09-929-924-18	Sequence 18, Appl
45	28	52.8	34	14	US-10-122-822-30	Sequence 30, Appl

Title: US-09-929-924-15
Perfect score: 53
Sequence: 1 VSEEQKVVQVVA 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 37674

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		%					
Result		Query					
No.	Score	Match	Length	DB	ID	Description	
1	33	62.3	86	2	G71636	acyl carrier prote	
2	33	62.3	86	2	A97848	acyl carrier prote	
3	31	58.5	99	2	S03525	T-cell receptor al	
4	30	56.6	76	2	T03810	hypothetical prote	
5	30	56.6	84	2	E64406	tetrahydromethanop	
6	30	56.6	96	2	T09310	thymidine kinase h	
7	29	54.7	21	2	S51066	ribosomal protein	
8	29	54.7	51	2	E97132	hypothetical prote	
9	29	54.7	75	2	H90187	SSU ribosomal prot	
10	29	54.7	89	2	T52484	ribosomal protein	
11	28	52.8	29	2	S39968	probable hydro-lya	
12	28	52.8	45	2	T52278	R2R3-MYB transcrip	
13	28	52.8	70	2	I49459	acetylcholine rece	
14	28	52.8	78	2	E97844	hypothetical prote	
15	28	52.8	83	2	H82356	conserved hypothet	
16	28	52.8	87	2	I40623	hypothetical prote	
17	28	52.8	87	2	D97109	uncharacterized co	
18	28	52.8	89	2	B46356	rev protein - simi	
19	28	52.8	90	2	D85627	hypothetical prote	
20	28	52.8	96	2	E69550	conserved hypothet	
21	28	52.8	98	2	C87404	ribosomal protein	
22	28	52.8	99	2	F64317	hypothetical prote	
23	27	50.9	52	2	S23750	phosphoenolpyruvat	
24	27	50.9	56	2	JW0072	phosphoenolpyruvat	

25	27	50.9	57	2	A39508	lipocortin IV - ra
26	27	50.9	58	2	S17700	hypothetical prote
27	27	50.9	58	2	T01101	hypothetical prote
28	27	50.9	60	2	S02189	hypothetical prote
29	27	50.9	62	2	C90870	hypothetical prote
30	27	50.9	62	2	AI0739	conserved hypothet
31	27	50.9	64	2	T36824	hypothetical prote
32	27	50.9	67	2	C84956	cell division prot
33	27	50.9	69	2	F64884	ydaC protein - Esc
34	27	50.9	73	2	D83949	hypothetical prote
35	27	50.9	86	2	F85748	unknown protein en
36	27	50.9	87	2	D69971	conserved hypothet
37	27	50.9	91	2	D86503	hypothetical prote
38	27	50.9	91	2	C72119	hypothetical prote
39	27	50.9	93	2	A33472	transcription regu
40	27	50.9	94	2	H95222	chaperonin, 10 kDa
41	27	50.9	94	2	A99087	cochaperonin GroES
42	27	50.9	97	2	S75011	hypothetical prote
43	27	50.9	98	2	AG1825	hypothetical prote
44	26	49.1	44	2	S40297	phosphoenolpyruvat
45	26	49.1	56	2	T03658	phosphoenolpyruvat

Title: US-09-929-924-15
 Perfect score: 53
 Sequence: 1 VSEEQKVVQVVA 12

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 15046

Minimum DB seq length: 0
 Maximum DB seq length: 100

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		%					
Result		Query					Description
No.	Score	Match	Length	DB	ID		
1	33	62.3	86	1	ACP_RICCN	Q92gd8	rickettsia
2	33	62.3	86	1	ACP_RICPR	Q9zch9	rickettsia
3	30	56.6	84	1	MTRG_METJA	Q58263	methanococc
4	29	54.7	80	1	CLVA_STYCL	P80710	styela clav
5	29	54.7	88	1	RS15_THETH	P80378	thermus the
6	29	54.7	91	1	RL31_PYRAE	Q8ztu2	pyrobaculum
7	29	54.7	95	1	RELX_ECOLI	Q60228	escherichia
8	28	52.8	80	1	COXK_PIG	Q8spj9	sus scrofa
9	28	52.8	87	1	YG97_CLOAB	P33660	clostridium
10	28	52.8	89	1	REV_SIVAG	P27981	simian immu
11	28	52.8	99	1	Y141_METJA	Q57606	methanococc
12	27	50.9	25	1	ACP_ALCFA	P80917	alcaligenes
13	27	50.9	60	1	PHX1_MOUSE	P15973	mus musculu
14	27	50.9	67	1	FTSL_BUCAI	P57318	buchnera ap
15	27	50.9	69	1	YDAC_ECOLI	P33230	escherichia
16	27	50.9	70	1	R17E_METKA	Q8tuz3	methanopyru
17	27	50.9	93	1	SP3D_BACSU	P15281	bacillus su
18	27	50.9	94	1	CH10_STRMT	Q8gbb7	streptococc
19	27	50.9	94	1	CH10_STROR	Q8kiy4	streptococc
20	27	50.9	94	1	CH10_STRPN	Q97nv3	streptococc
21	27	50.9	94	1	CH10_STRR6	Q8cwn9	streptococc
22	26	49.1	23	1	COXK_CANFA	Q9trz8	canis famil
23	26	49.1	25	1	ACP_ACICA	P80916	acinetobact
24	26	49.1	29	1	COXK_SHEEP	Q9tr28	ovis aries
25	26	49.1	42	1	Y16N_BPT4	P39249	bacterioph
26	26	49.1	69	1	YQ12_VIBCH	Q9knw8	vibrio chol
27	26	49.1	74	1	MTRG_METKA	O32868	methanopyru
28	26	49.1	79	1	ACP1_RALSO	Q8y0j1	ralstonia s

29	26	49.1	80	1	CLVC_STYCL	018493	styela clav
30	26	49.1	80	1	COXK_BOVIN	P07470	bos taurus
31	26	49.1	80	1	COXK_MOUSE	P56392	mus musculu
32	26	49.1	81	1	ACP_RHOBA	Q7uyy2	rhodopirell
33	26	49.1	84	1	YD33_METJA	Q58729	methanococc
34	26	49.1	99	1	PYRG_MYCCC	Q93dw6	mycoplasma
35	25	47.2	19	1	FIBB_VULVU	P14482	vulpes vulp
36	25	47.2	31	1	FIBB_CANFA	P02677	canis famil
37	25	47.2	37	1	RL36_MYCGA	Q9rdv9	mycoplasma
38	25	47.2	50	1	OM05_YEAST	P80967	saccharomyc
39	25	47.2	56	1	YD96_HAEIN	P44174	haemophilus
40	25	47.2	60	1	YG9A_CLOTE	P60083	clostridium
41	25	47.2	63	1	ITR4_LUFCY	P34950	luffa cylin
42	25	47.2	66	1	Y828_METJA	Q58238	methanococc
43	25	47.2	67	1	Y737_ARCFU	O29521	archaeoglob
44	25	47.2	70	1	SIX1_LEIQU	P19856	leiurus qui
45	25	47.2	70	1	YD20_VIBVU	Q8dcs6	vibrio vuln

Title: US-09-929-924-15
 Perfect score: 53
 Sequence: 1 VSEEQKVVQVVA 12

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 175362

Minimum DB seq length: 0
 Maximum DB seq length: 100

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : SPTREMBL_25:*
 1: sp_archaea:*
 2: sp_bacteria:*
 3: sp_fungi:*
 4: sp_human:*
 5: sp_invertebrate:*
 6: sp_mammal:*
 7: sp_mhc:*
 8: sp_organelle:*
 9: sp_phage:*
 10: sp_plant:*
 11: sp_rodent:*
 12: sp_virus:*
 13: sp_vertebrate:*
 14: sp_unclassified:*
 15: sp_rvirus:*
 16: sp_bacteriap:*
 17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result						Description
	No.	Score	Match	Length	ID	
	1	53	100.0	90	11 P70443	P70443 mus musculu
	2	35	66.0	83	9 Q853T7	Q853t7 mycobacteri
	3	30	56.6	42	10 Q9XIT8	Q9xit8 glycine max
	4	30	56.6	54	16 Q8E8H3	Q8e8h3 shewanella
	5	30	56.6	61	12 Q91TV0	Q91tv0 tupaia herp
	6	30	56.6	74	12 Q91FM3	Q91fm3 chilo iride
	7	30	56.6	76	10 P93382	P93382 nicotiana t
	8	30	56.6	82	16 Q8G4U1	Q8g4u1 bifidobacte
	9	30	56.6	88	16 Q7U8N9	Q7u8n9 synechococc
	10	30	56.6	96	12 Q69040	Q69040 human herpe
	11	29	54.7	45	10 O49777	O49777 arabidopsis

12	29	54.7	51	16	Q97HX2	Q97hx2 clostridium
13	29	54.7	54	5	Q9TWZ0	Q9twz0 paramecium
14	29	54.7	54	16	Q8DTS1	Q8dts1 streptococc
15	29	54.7	74	16	Q83RL2	Q83rl2 shigella fl
16	29	54.7	75	17	Q97ZY7	Q97zy7 sulfolobus
17	29	54.7	84	6	Q8HXQ8	Q8hxq8 equus cabal
18	29	54.7	94	10	Q9LI12	Q9li12 oryza sativ
19	29	54.7	94	16	Q8ETP6	Q8etp6 oceanobacil
20	29	54.7	95	2	Q8VU40	Q8vu40 escherichia
21	29	54.7	100	16	Q8RE20	Q8re20 fusobacteri
22	28	52.8	29	2	Q54200	Q54200 streptomyce
23	28	52.8	31	6	Q8WP10	Q8wp10 ateles belz
24	28	52.8	42	10	Q9XIT4	Q9xit4 glycine max
25	28	52.8	42	10	Q9LE64	Q9le64 adiantum ra
26	28	52.8	42	10	Q9LE26	Q9le26 psilotum nu
27	28	52.8	43	10	Q9SQC6	Q9sqc6 zea mays (m
28	28	52.8	45	10	Q8L6M4	Q8l6m4 gossypium h
29	28	52.8	45	10	Q8L6L9	Q8l6l9 gossypium h
30	28	52.8	45	10	O49755	O49755 arabidopsis
31	28	52.8	45	10	Q84U47	Q84u47 dendrobium
32	28	52.8	53	16	Q8R6R2	Q8r6r2 thermoanaer
33	28	52.8	63	6	Q9XT66	Q9xt66 canis famil
34	28	52.8	65	17	Q977C3	Q977c3 sulfolobus
35	28	52.8	78	16	Q92GG6	Q92gg6 rickettsia
36	28	52.8	79	2	Q84B18	Q84b18 streptococc
37	28	52.8	83	16	Q9KVI3	Q9kvi3 vibrio chol
38	28	52.8	85	16	Q89GQ9	Q89gq9 bradyrhizob
39	28	52.8	86	13	Q7SZL4	Q7szl4 oryzias lat
40	28	52.8	87	10	Q8S428	Q8s428 zea mays (m
41	28	52.8	87	10	Q8S433	Q8s433 sorghum bic
42	28	52.8	90	16	Q8X4I1	Q8x4i1 escherichia
43	28	52.8	91	5	Q8MQ96	Q8mq96 caenorhabdi
44	28	52.8	95	16	Q9RJN7	Q9rjn7 streptomyce
45	28	52.8	96	17	O30267	O30267 archaeoglob